

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 5, 2005, 21:57:00 ; Search time 5915 Seconds  
(without alignments)  
10993.559 Million cell updates/sec

Title: US-09-640-582A-1  
Perfect score: 1342  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues 9416466  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1335.6	99.5	1342	6	AX018991 Sequence
2	1297	96.6	3372	6	AX211346 Sequence
3	1297	96.6	3372	9	AF065164 Homo sapi
4	1295.4	96.5	3459	6	AX348086 Sequence
5	1295.4	96.5	3459	9	AF064877 Homo sapi
6	1208	90.0	1792	6	AR483555 Sequence
7	1207	89.9	1792	6	AR483555 Sequence
8	1194.8	89.0	105108	2	AC139548 Homo sapi
9	1194.8	89.0	133193	2	AC139548 Homo sapi
10	1194.8	89.0	199198	9	AC021413 Homo sapi
11	1194.4	89.0	1790	6	BD139757 Ion chann
12	1194.4	89.0	1790	6	AR307665 Sequence
13	1193.2	88.9	127422	2	AC136294 Homo sapi
14	1192.6	88.9	163776	2	AC135994 Homo sapi
15	1191.6	88.8	2125	6	AX647819 Sequence
16	1191.6	88.8	123089	9	AC135731 Homo sapi
17	1191.6	88.8	123233	3	AC135625 Homo sapi
18	1191.6	88.8	158033	2	AC135991 Homo sapi
19	1191.6	88.8	164711	2	AC139564 Homo sapi

c	20	1191.6	88.8	166484	2	AC026830 Homo sapi
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	22	1191.6	88.8	188448	9	AC139426 Homo sapi
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	24	1074.2	80.0	2633	10	AB164197 Rattus no
	25	1071	79.8	2511	10	AF247451 Rattus no
	26	1048.6	78.1	3102	6	AX211350 Sequence
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ALIGNMENTS

RESULT 1  
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LOCUS AX018991 1342 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 1 from Patent WO942574.  
ACCESSION AX018991  
VERSION AX018991.1 GI:10043084  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1  
AUTHORS Baumann,A., Gauss,R., Kaupp,B., Boenigk,W., Scholten,A. and Seifert,R.  
TITLE Sequences of an ih ionic channel and the use thereof  
JOURNAL Patent: WO 942574-A 1 26-AUG-1999;  
BAUMANN ARND (DE); GAUSS RENATE (DE); KAUPP BENJAMIN (DE); BOENIGK WOLFGANG (DE); KERNFORSCHUNGSANLAGE JUELICH (DE); SCHOLTEN ALEXANDER (DE); SEIFERT REINHARD (DE)

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RESULT 3  
AF065164 3372 bp mRNA linear PRI 15-OCT-1999  
LOCUS Homo sapiens hyperpolarization-activated, cyclic nucleotide-gated  
DEFINITION channel 2 (HCN2) mRNA, complete cds.  
ACCESSION AF065164  
VERSION AF065164.2 GI:4996893  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 3372)  
AUTHORS Vaccari, A., Moroni, A., Rocchi, M., Gorza, L., Bianchi, M.E.,  
Beltrame, M. and DiFrancesco, D.  
TITLE The human gene coding for HCN2, a pacemaker channel of the heart  
JOURNAL Biochim. Biophys. Acta 1446 (3), 419-425 (1999)

99453744 MEDLINE  
10524219 PUBMED  
2 (bases 1 to 3372) REFERENCE  
Moroni, A., Vaccari, T., Beltrame, M., Bianchi, M.E. and DiFrancesco, D.  
Direct Submission  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
3 (bases 1 to 3372)  
Moroni, A., Vaccari, T., Beltrame, M., Bianchi, M.E. and DiFrancesco, D.  
Direct Submission  
AUTHORS  
TITLE  
JOURNAL  
REMARK  
SEQUENCE UPDATE BY SUBMITTER  
REFERENCE  
4 (bases 1 to 3372)  
Moroni, A., Vaccari, T., Beltrame, M., Bianchi, M.E. and DiFrancesco, D.  
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AUTHORS  
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REMARK  
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ORIGIN

Query Match 96.6%; Score 1297; DB 9; Length 3372;  
Best Local Similarity 99.0%; Pred. No. 1.8e-164;  
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DEFINITION Sequence 3 from Patent WO0202630.  
ACCESSION AX348086  
VERSION AX348086.1 GI:18614193  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Strijbos, P.J., Bates, S.G., Gloger, I.G. and Davies, C.G.  
TITLE New use  
JOURNAL Patent: WO 0202630-A 3 10-JAN-2002;  
SMITHKLINE BEECHAM PLC (GB)  
FEATURES  
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Best Local Similarity 99.0%; Pred. No. 2.9e-164;  
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RESULT 6  
AF064877  
LOCUS AF064877 1792 bp mRNA linear PRI 29-MAY-1998  
DEFINITION Homo sapiens ion channel BCNG-2 mRNA, partial cds.  
ACCESSION AF064877  
VERSION AF064877.1 GI:3168875  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1792)  
Santor, B., Grant, S.G., Bartsch, D. and Kandel, E.R.  
Interactive cloning with the SH3 domain of N-src identifies a new  
brain specific ion channel protein, with homology to eag and cyclic  
nucleotide-gated channels  
Proc. Natl. Acad. Sci. U.S.A. 94 (26), 14815-14820 (1997)  
98070835  
9405696  
2 (bases 1 to 1792)  
Santor, B., Liu, D.T., Yao, H., Bartsch, D., Kandel, E.R.,  
Siegelbaum, S.A. and Tibbs, G.R.  
Identification of a gene encoding a hyperpolarization-activated  
pacemaker channel of brain  
Cell 93 (5), 717-729 (1998)  
98292171  
9630217  
3 (bases 1 to 1792)  
Santor, B., Liu, D.T., Yao, H., Bartsch, D., Kandel, E.R.,  
Siegelbaum, S.A. and Tibbs, G.R.  
Direct Submission  
Submitted (14-MAY-1998) Center for Neurobiology and Behavior,  
Columbia University, 722 West 168th Street, New York, NY 10032, USA  
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ORIGIN

Query Match 90.0%; Score 1208; DB 9; Length 1792;  
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Matches 1236; Conservative 0; Mismatches 10; Indels 2; Gaps 2;  
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DEFINITION	Homo sapiens chromosome 15 clone RP13-972E7 map 15, WORKING DRAFT		
ACCESSION	AC139689		
VERSION	HTG139689.2 GI:28467241		
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Birren, B., Nusbaum, C. and Lander, E.		
JOURNAL	Homo sapiens chromosome 15, clone RP13-972E7		
REFERENCE	1 (bases 1 to 105108)		
AUTHORS	Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguelavkiy, L., Boukhalter, B., Camarata, J., Chang, J., Choepel, Y., Collamore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (09-FEB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
AUTHORS	3 (bases 1 to 105108)		
REFERENCE	Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguelavkiy, L., Boukhalter, B., Camarata, J., Chang, J., Choepel, Y.,		

Collamore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.			
Center: Whitehead Institute/ MIT Center for Genome Research			
Center code: WIBR			
Web site: http://www-seq.wi.mit.edu			
Contact: sequence_submissions@genome.wi.mit.edu			
Project Information			
Center project name: L29405			
Center clone name: 972_E7			
Sequencing vector: Plasmid; n/a; 100% of reads			
Chemistry: Dye-terminator Big Dye; 100% of reads			
Assembly program: Phrap; version 0.960731			
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Insert size: 103708; sum-of-contigs			
Quality coverage: 15.9 in Q20 bases; agarose-fp			
Quality coverage: 21.5 in Q20 bases; sum-of-contigs			
NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.			
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9814	9913: gap of 100 bp		
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18399	18498: gap of 100 bp		
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27321	27420: gap of 100 bp		
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	37462	37561: gap of 100 bp	bp in length
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*	37562	49587: gap of 100 bp	
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## RESULT 9

## AC139548

## LOCUS DEFINITION

AC139548 Homo sapiens chromosome 15 clone RP13-642K1 map 15, WORKING DRAFT SEQUENCE, 17 unordered pieces.

## AC139548

## AC139548.2

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

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## AUTHORS

Center project name: L29456  
Center clone name: 642\_K1  
Sequencing vector: Plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 127247 bases at least Q40  
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Insert size: 131593; sum-of-contigs  
Quality coverage: 21.9 in Q20 bases; agarose-fp  
Quality coverage: 22.9 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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Homo sapiens chromosome 15 clone RP13-642K1 map 15, WORKING DRAFT  
SEQUENCE, 17 unordered pieces.  
AC139548  
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HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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Unpublished  
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Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,  
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,  
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,  
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
Roman,J., Schauer,S., Schupack,R., Seaman,S., Severy,P., Smith,C.,  
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,  
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,  
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,  
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (05-FEB-2003) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 133193)  
Birren,B., Nuebaum,C., Lander,E., Abouelleil,A., Allen,N.,  
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,  
Boguelavkiy,L., Boukgalter,B., Camarata,J., Chang,J., Choepel,Y.,  
Collamore,A., Cook,A., Cooke,P., Corum,B., DeArelano,K.,  
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,  
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,  
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,  
Hall,J., Horton,L., Hulne,W., Iliev,I., Johnson,R., Jones,C.,  
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,  
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,  
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Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,  
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,  
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Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
Roman,J., Schauer,S., Schupack,R., Seaman,S., Severy,P., Smith,C.,  
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,  
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,  
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Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (21-FEB-2003) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Feb 21, 2003 this sequence version replaced gi:28209588.  
All repeats were identified using RepeatMasker:  
Smit,A.F.A. & Green,P. (1996-1997)  
http://ftp.genome.washington.edu/RW/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu

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DEFINITION AC021413  
ACCESSION AC021413  
VERSION AC021413.16 GI:27476161  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 199198)  
AUTHORS Birren,B., Nusbaum,C. and Lander,E.  
TITLE Homo sapiens chromosome 15, clone RP11-30N16  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 199198)  
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavskiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Collangelo, M., Collins, S., Collymore, A., Cooke, P., DeArrellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczy, J., Levine, R., Lieu, G., Liu, G., Locke, K., MacDonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Oliver, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 199198)

**TITLE**  
JOURNAL  
**REFERENCE**  
**AUTHORS**

Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavskiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Collangelo, M., Collins, S., Collymore, A., Cooke, P., DeArrellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczy, J., Levine, R., Lieu, G., Liu, G., Locke, K., MacDonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Oliver, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (21-NOV-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
4 (bases 1 to 199198)

**TITLE**  
JOURNAL  
**REFERENCE**  
**AUTHORS**

Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavskiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Collangelo, M., Collins, S., Collymore, A., Cooke, P., DeArrellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczy, J., Levine, R., Lieu, G., Liu, G., Locke, K., MacDonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Oliver, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (03-JAN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jan 3, 2003 this sequence version replaced gi:25102383.  
All repeats were identified using RepeatMasker:  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
http://www-seq.wi.mit.edu

**TITLE**  
JOURNAL  
**COMMENT**

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Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information -----



ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 1790)  
AUTHORS Kandel,E.R., Santoro,B., Bartsch,D., Siegelbaum,S., Tibbs,G. and Grant,S.  
TITLE Ion channel compound gated by brain or heart cyclic nucleotide and utilization thereof  
JOURNAL Patent: JP 2002508930-A 4 26-MAR-2002;  
COMMENT THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK  
OS Linear  
PN JP 2002508930-A/4  
PD 26-MAR-2002  
PF 23-DEC-1998 JP 2000525534  
PR 23-DEC-1997 US 08/997685,28-MAY-1998 US 09/086436 PI  
ERIC R KANDEL,BINA SANTORO,DUSAN BARTSCH,STEVEN SIEGELBAUM, PI  
GARETH TIBBS,  
PI SETH GRANT  
PC C12N15/09,A61K9/08,A61K9/12,A61K9/16,A61K9/20,A61K45/00 PC  
,A61P9/00,A61P25/08,  
PC A61P25/16,A61P25/28,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC  
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Best Local Similarity 98.9%; Pred. No. 1.1e-150;  
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AR307665  
LOCUS AR307665  
DEFINITION Sequence 11 from patent US 6551821.  
ACCESSION AR307665  
VERSION AR307665.1 GI:31698370  
KEYWORDS SOURCE  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 1790)  
Kandel,E.R., Santoro,B., Bartsch,D., Siegelbaum,S., Tibbs,G. and Grant,S.  
TITLE Brain cyclic nucleotide gated ion channel and uses thereof  
JOURNAL Patent: US 6551821-A 11 22-APR-2003;  
FEATURES Location/Qualifiers  
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VERSION	AC136294.4		
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SOURCE	Homo sapiens (human)		
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AUTHORS	Birren, B., Nusbaum, C. and Lander, E.		
TITLE	Homo sapiens chromosome 15, clone CTD-209012		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 127422)		
AUTHORS	Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgaltier, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gordon, L., Huh, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Melrim, J., Meneus, L., Mihova, T., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talmas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.		
TITLE	Submitted (31-OCT-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
JOURNAL	3 (bases 1 to 127422)		
AUTHORS	Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgaltier, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gordon, L., Huh, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Melrim, J., Meneus, L., Mihova, T., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talmas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.		

Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K.,  
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Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jan 1, 2003 this sequence version replaced gi:27356717.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
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----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L28512  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 2 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
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DEFINITION AC135994  
ACCESSION AC135994  
VERSION AC135994.6 GI:27369446



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ORGANISM      Homo sapiens
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AUTHORS      Suwa, M., Arai, K., Akiyama, Y. and Aburatani, H.
TITLE      Guanosine triphosphate-binding protein coupled receptors
JOURNAL      Patent: EP 1270724-A 2011 02-JAN-2003;
              National Institute of Advanced Industrial Science and Technology
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Listing first 45 summaries

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3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1335.6	99.5	1342	2	AZ09482 Human Ih
2	1297	96.6	3372	4	Ah48729 Human HCN
3	1297	96.6	3372	13	Adg83419 Human tum
4	1295.4	96.5	3459	6	Aad29756 Human hyp
5	1194.4	89.0	1790	2	Aax84445 Human bra
6	1191.6	88.8	2125	10	Adc87558 Human GPC
7	1113.2	83.0	3431	4	Aah98302 Human EST
8	1048.6	78.1	3102	4	Aah48731 Murine HC
9	1032.4	76.9	1820	2	Aaz09488 Bovine re
10	992.4	73.9	2886	2	Aaz09491 Human Ih
11	927.2	69.1	4751	2	Aaz09496 Human hea
12	927.2	69.1	4751	6	Aad29757 Human hyp
13	927.2	69.1	5065	4	Aah48730 Human HCN
14	927.2	69.1	5065	13	Adr86593 Human HCN
15	927.2	69.1	5499	4	Aba09197 Human cat
16	871	64.9	1584	2	Aax84444 Mouse bra
17	753.4	56.1	3852	6	Aal44691 Human tra
18	753	56.1	2340	6	Abk86386 Human HCN
19	751.8	56.0	2217	8	Abx71090 Novel hum
20	751.8	56.0	2325	3	Aac66779 Human hyp

21	751.8	56.0	2325	8	Abz75841	Human HCN
22	751.8	56.0	2325	8	Abz58682	Human HCN
23	751.8	56.0	2325	8	ACA61916	cDNA enco
24	751.8	56.0	2325	10	ABX95515	CDNA enco
25	751.8	56.0	3496	6	Aad29758	Human hyp
26	751.8	56.0	3601	12	ADQ83229	Human tum
27	751.8	56.0	3601	13	ADQ85140	Human tum
28	751.4	56.0	2340	6	ABK86387	Human HCN
29	751.4	56.0	2340	6	ABK86385	Human HCN
30	735.2	54.8	2733	2	Aax84442	Mouse bra
31	720.8	53.7	3112	2	Aaz09483	Rat ol fac
32	688.8	51.3	1507	2	AAx84446	Mouse bra
33	681.8	50.8	2990	10	ADJ95123	Novel NOV
34	680.2	50.7	1873	6	AAx18224	Human PCR
35	680.2	50.7	1873	6	AAx18223	Human PCR
36	680.2	50.7	2263	2	AAx84443	Human bra
37	680.2	50.7	2670	6	Aad29755	Human hyp
38	680.2	50.7	2673	8	ABZ75836	Human HCN
39	680.2	50.7	2673	8	ABZ58677	Human HCN
40	680.2	50.7	2673	8	ACA61911	cDNA enco
41	680.2	50.7	2673	10	ABX95510	CDNA enco
42	680.2	50.7	2748	6	ABT09623	Human HCN
43	680.2	50.7	2748	6	ABT09624	Human HCN
44	680.2	50.7	2748	6	ABT09630	Human HCN
45	680.2	50.7	2748	6	ABT09629	Human HCN

ALIGNMENTS

RESULT 1

AZ09482

ID AAZ09482 standard; DNA; 1342 BP.

XX AAZ09482;

XX 02-NOV-1999 (first entry)

XX Human Ih ion channel DNA fragment.

XX Ih ion channel; human; sea urchin; fruit fly; rat; bovine; analgesic;  
KW cardioactive; pacemaker; cardiac muscle; ion channel modulator;  
KW treatment; diagnosis; ion channel-related disease; cardiac disease;  
KW circulatory disorder; sinus ganglion regulation; sleep disorder;  
KW cortico-thalamic neuron; pain; detection; mutation; ss.  
XX Homo sapiens.  
XX WO9942574-A1.  
XX 26-AUG-1999.  
XX 12-FEB-1999; 99WO-EP000942.  
XX 17-FEB-1998; 98DE-01006581.  
XX (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.  
XX Baumann A, Boenigk W, Gause R, Scholten A, Seifert R, Kaupp B;  
XX WPI; 1999-527472/44.  
XX New nucleic acid encoding an Ih ion channel, used to identify specific  
XX modulators, and for treatment, prevention and diagnosis of e.g. cardiac  
XX disease.  
XX Claim 3; Page 57; 82pp: German.  
XX This invention describes a novel Ih ion channel, isolated from human, sea  
XX urchin, bovine, rat, and fruitfly. The ion channels of the invention have  
XX analgesic and cardioactive activity. The Ih ion channel participates in  
XX the pacemaker function in cardiac muscle. The Ih ion channel nucleic acid  
XX and its encoding protein is used to identify substances (A) that modulate

CC activity of ion channels; to treat and/or diagnose ion channel-related  
CC diseases, particularly cardiac or circulatory disorders and to prevent  
CC and/or treat cardiac/circulatory disorders (especially faulty regulation  
CC of the sinus ganglion), sleep disorders (particularly abnormal function  
CC of cortico-thalamic neurons) and/or pain. Fragments of the Ih ion channel  
CC nucleic acid are used to detect mutations e.g. for differential  
CC diagnosis. This sequence encodes a human Ih channel fragment isolated  
CC from human thalamus tissue  
XX

SQ Sequence 1342 BP; 252 A; 451 C; 390 G; 240 T; 0 U; 9 Other;

Query Match 99.5%; Score 1335.6; DB 2; Length 1342;  
Best Local Similarity 100.0%; Pred. No. 3.4e-229;  
Matches 1342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTGGCTTCAACCAAGATCTCTCAGCCTCTCTGGGCTGTGGCTCTTCCAGCCTTATCC 60  
DB 1 CGTTGGCTTCAACCAAGATCTCTCAGCCTCTCTGGGCTGTGGCTCTTCCAGCCTTATCC 60  
QY 61 GCTACATCATCTAGTGGAGGAGATCTTCCATGACCTTATGACCTGGCCAGCGGGTGA 120  
DB 61 GCTACATCATCTAGTGGAGGAGATCTTCCATGACCTTATGACCTGGCCAGCGGGTGA 120  
QY 121 TGAGGATCTGCAATCTCATCAGCATGATCTGTCTGTCTGCCACTGGGACGGCTGCTGC 180  
DB 121 TGAGGATCTGCAATCTCATCAGCATGATCTGTCTGTCTGCCACTGGGACGGCTGCTGC 180  
QY 181 AGTTCTGTGGTCCCATGCTGCGAGACTTCCCGCGCAACTGCTGGGTGCCATCAATGGCA 240  
DB 181 AGTTCTGTGGTCCCATGCTGCGAGACTTCCCGCGCAACTGCTGGGTGCCATCAATGGCA 240  
QY 241 TGGTGAACCACTCTGTGGAGTGAATCTTCTTCTGCACTTCCAGGCGCATGAGCCACA 300  
DB 241 TGGTGAACCACTCTGTGGAGTGAATCTTCTTCTGCACTTCCAGGCGCATGAGCCACA 300  
QY 301 TGTCTGTGATCGGGTACGGCGGCGAGGATGATGCGGATGATGCGGATGATGCGGATGATG 360  
DB 301 TGTCTGTGATCGGGTACGGCGGCGAGGATGATGCGGATGATGCGGATGATGCGGATGATG 360  
QY 361 TGTCTGAGCATGATGTTGGGTGCGACCTGTCTAGCCATGTTCTGCGCCACGCGCTGCCC 420  
DB 361 TGTCTGAGCATGATGTTGGGTGCGACCTGTCTAGCCATGTTCTGCGCCACGCGCTGCCC 420  
QY 421 TCATCAGTCTGTGGATCTCTCGCGGCGGCGAGTACCGAGGAGTACAGGAGTGGAGC 480  
DB 421 TCATCAGTCTGTGGATCTCTCGCGGCGGCGAGTACCGAGGAGTACAGGAGTGGAGC 480  
QY 481 AGTACATGTCCTTCCCAAGCTGCGAGTCTTCCCGCAGAGATCCACGACTACTATG 540  
DB 481 AGTACATGTCCTTCCCAAGCTGCGAGTCTTCCCGCAGAGATCCACGACTACTATG 540  
QY 541 AGCACCCTTACCGAGGCAAGATGTTTGAAGGACAGCATCTTGGCGAGCTCAACGGGC 600  
DB 541 AGCACCCTTACCGAGGCAAGATGTTTGAAGGACAGCATCTTGGCGAGCTCAACGGGC 600  
QY 601 CCTTGGGAGGAGATCGTCAACTTCACTGCGGAGCTGTGGCTTCCATGCGGCTGT 660  
DB 601 CCTTGGGAGGAGATCGTCAACTTCACTGCGGAGCTGTGGCTTCCATGCGGCTGT 660  
QY 661 TGGCCAAACCGGACCCCACTTCTGTCAGCGCATGCTGACCAAGCTCAAGTTTCGAGGCT 720  
DB 661 TGGCCAAACCGGACCCCACTTCTGTCAGCGCATGCTGACCAAGCTCAAGTTTCGAGGCT 720  
QY 721 TCCAGCGGGTGAATCATCATCGCGAAGGACCATCGGAGAGATGTACTTTCATCC 780  
DB 721 TCCAGCGGGTGAATCATCATCGCGAAGGACCATCGGAGAGATGTACTTTCATCC 780  
QY 781 AGCAGCGGCTGTGCTGCTGCTCACTAAGGCGCAAGAGAGATGAGCTGTCGATGGCT 840  
DB 781 AGCAGCGGCTGTGCTGCTGCTCACTAAGGCGCAAGAGAGATGAGCTGTCGATGGCT 840  
QY 841 CTTACTTTCGGGAGATCTGCTGCTCATCCCGGGCGCGCAGCGGAGCTGCGGGCTG 900

DB 841 CCTACTTCGGGGAGATCTGCTGCTCAACCCGGGGCGCGACGCGAGCGTGGGGCTG 900  
QY 901 ACACCTACTGCGGCTCTTATTCGCTGAGGCTGGGACAACTTCAACGAGTGTCTGGAGGAGT 960  
DB 901 ACACCTACTGCGGCTCTTATTCGCTGAGGCTGGGACAACTTCAACGAGTGTCTGGAGGAGT 960  
QY 961 ACCCCATCATGCGGCGGCTTTCGAGAGCGGTGGCCATCGACCGCTTGAACCCATCGGCA 1020  
DB 961 ACCCCATCATGCGGCGGCTTTCGAGAGCGGTGGCCATCGACCGCTTGAACCCATCGGCA 1020  
QY 1021 AGAAGATTTCCATCTCTCTGCAACAGGTGCGAGCATGACCTCAACTCGGGCGTATTCAACA 1080  
DB 1021 AGAAGATTTCCATCTCTCTGCAACAGGTGCGAGCATGACCTCAACTCGGGCGTATTCAACA 1080  
QY 1081 ACCGAGGAACGCCCATCATCCAGGAGATCGTCAAGTACGACCGCGAGATGTTGCGAGGAG 1140  
DB 1081 ACCGAGGAACGCCCATCATCCAGGAGATCGTCAAGTACGACCGCGAGATGTTGCGAGGAG 1140  
QY 1141 CGGAGCTGGGCTCAGCGGTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1200  
DB 1141 CGGAGCTGGGCTCAGCGGTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1200  
QY 1201 CGGCAATCGCCACGCTGCGAGGCGGCGGCGCATGAGCTTCTGCGCGCGAGTGGCGGCG 1260  
DB 1201 CGGCAATCGCCACGCTGCGAGGCGGCGGCGCATGAGCTTCTGCGCGCGAGTGGCGGCG 1260  
QY 1261 GCTCGTGGGCGGCTGCGGCTGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1320  
DB 1261 GCTCGTGGGCGGCTGCGGCTGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1320  
QY 1321 CGCACTGCHGCCNCTCACCC 1342  
DB 1321 CGCACTGCHGCCNCTCACCC 1342

RESULT 2

AAH48729  
ID AAH48729 standard; cdna; 3372 BP.  
XX AC AAH48729;  
XX DT 26-OCT-2001 (first entry)  
XX DE Human HCN2 cdna.  
XX KW Human; activator; patch-clamp; high through-put screening; inhibitor;  
KW hyperpolarization-activated cation channel; HCN2; ss.  
XX OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 36..2705  
FT /\*tag= a  
FT /product= "HCN2"  
XX WO200159153-A2.  
XX PD 16-AUG-2001.  
XX PF 24-JAN-2001; 2001WO-EP000755.  
XX PR 12-FEB-2000; 2000DE-01006309.  
XX PA (AVET ) AVENTIS PHARMA DEUT GMBH.  
XX Jansen H, Brueggemann A, Heitsch H, Goegelstein H;  
DR WPI; 2001-550023/61.  
DR P-PSDB; AAB86461.  
PT Identifying substances which modify activity of hyperpolarization-  
PT activated cation channels using fluorescent imaging is useful to identify  
PT possible therapeutic pharmaceuticals.



XX Claim 1; SEQ ID NO 233; 5504pp; English.

PS The present invention describes an isolated tumour-associated antigenic

XX target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide

CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of

CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%

CC sequence identity to (a) - (c); or (e) a sequence that hybridises to (a) -

CC (c). Also described: (1) an expression vector comprising the above

CC nucleic acid; (2) a host cell comprising the above expression vector; (3)

CC a process for producing a polypeptide; (4) an isolated polypeptide

CC comprising: (a) an amino acid sequence encoded by any of the above

CC nucleotide sequences; (b) an amino acid sequence encoded by the full-

CC length coding region of the above nucleotide sequences; or (c) a sequence

CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide

CC comprising the above polypeptide fused to a heterologous polypeptide; (6)

CC an isolated antibody that binds to the above polypeptide; (7) a process

CC for producing the antibody; (8) an isolated oligopeptide that binds to

CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)

CC binding organic molecule that binds to the above polypeptide; (10) a

CC composition of matter comprising the above (chimeric) polypeptide,

CC antibody, oligopeptide or TAT binding organic molecule, in combination

CC with a carrier; (11) an article of manufacture comprising a container and

CC the composition of matter contained within the container; (12) methods of

CC inhibiting the growth of a cell that expresses the above protein, where

CC the growth of the cell is at least in part dependent upon a growth

CC potentiating effect of the above protein; (13) a method of

CC therapeutically treating a mammal having a cancerous tumour comprising

CC cells that express the above protein; (14) a method of determining the

CC presence of a protein in a sample suspected of containing the protein

CC described above; (15) methods of diagnosing the presence of a tumour in a

CC mammal; (16) a method for treating or preventing a cell proliferative

CC disorder associated with increased expression or activity of the above

CC protein; and (17) a method of binding an antibody, oligopeptide or

CC organic molecule to a cell that expresses the protein described above.

CC The TAT sequences have cytostatic activities, and can be used in gene

CC therapy. The composition and methods are useful for diagnosing,

CC preventing or treating cancer. The composition is also used for preparing

CC a medicament for the therapeutic treatment or diagnostic detection of a

CC cell proliferative disorder or cancer. The present sequence represents a

CC human TAT cDNA sequence from the present invention.

XX

SQ Sequence 3372 BP; 512 A; 1305 C; 1078 G; 477 T; 0 U; 0 Other;

Query Match 96.8%; Score 1297; DB 13; Length 3372;

Best Local Similarity 99.0%; Pred. No. 2.8e-222;

Matches 1328; Conservative 7; Mismatches 3; Indels 3; Gaps 3;

QY 4 TGGGCTTACCAAGATCCTCAGGCTCTCGGGCTGCTGGGCTCTCAGCGCTGATCCGCT 63

DB 1012 TGGGCTTACCAAGATCCTCAGGCTCTCGGGCTGCTGGGCTCTCAGCGCTGATCCGCT 1071

QY 64 ACATCCATCAGTGGGAGGAGATCTCCACATGACCTATGACCTGGCCAGCGGGTGA 123

DB 1072 ACATCCATCAGTGGGAGGAGATCTCCACATGACCTATGACCTGGCCAGCGGGTGA 1131

QY 124 GATCTGCAATCTCATCAGATGATCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 183

DB 1132 GATCTGCAATCTCATCAGATGATCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1191

QY 184 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 243

DB 1192 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1251

QY 244 TGAACCACTCGTGGAGTGAATCTACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 303

DB 1252 TGAACCACTCGTGGAGTGAATCTACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1311

QY 304 TGTGATCGGGTACGGCGGCGAGGCGCGGAGAGATGACGACATCTGGCTGACCATGC 363

DB 1312 TGTGATCGGGTACGGCGGCGAGGCGCGGAGAGATGACGACATCTGGCTGACCATGC 1371

QY 364 TCAGCATGATTGGGGTGCCACCTGTACGCCATGTTTCATCGGCCACGCCACTGCCCTCA 423

DB 1372 TCAGCATGATTGGGGTGCCACCTGTAGCCATGTTTCATCGGCCACGCCACTGCCCTCA 1431

QY 424 TCCAGTCTCTGAGATCTCTCGGGGCGCCAGTACAGGAGAAATACAGCAGGTGGAGCAGT 483

DB 1432 TCCAGTCTCTGAGATCTCTCGGGGCGCCAGTACAGGAGAAATACAGCAGGTGGAGCAGT 1491

QY 484 ACATGCTCTCCACAAAGCTGCGAGCTGCTCCGCGCAGAAATCCACGACTACTATGAGC 543

DB 1492 ACATGCTCTTCACAAAGCTGCGAGCTGCTCCGCGCAGAAATCCACGACTACTATGAGC 1551

QY 544 ACCGTTACAGGGCAAGATGTTTGAACGAGGACAGCATCTCGGGGAGCTCAACCGGCCCC 603

DB 1552 ACCGTTACAGGGCAAGATGTTTGAACGAGGACAGCATCTCGGGGAGCTCAACCGGCCCC 1611

QY 604 TCGCGGAGGAGATCGTCAACTTCAACTCGCGGAGCTGGTGGCTTCCATCGCGCTGTTCCG 663

DB 1612 TCGCGGAGGAGATCGTCAACTTCAACTCGCGGAGCTGGTGGCTTCCATCGCGCTGTTCCG 1671

QY 664 CCAACGCGGACCCCAACTTCTGTCAGGCGCATGCTGACCAAGCTCAAGTTTCAGAGTCTTCC 723

DB 1672 CCAACGCGGACCCCAACTTCTGTCAGGCGCATGCTGACCAAGCTCAAGTTTCAGAGTCTTCC 1731

QY 724 AGCCGGGTGACTACATCATCTCCGCGAAGGACCATCGGGAAGAGATGACTTTCATCCAGC 783

DB 1732 AGCCGGGTGACTACATCATCTCCGCGAAGGACCATCGGGAAGAGATGACTTTCATCCAGC 1791

QY 784 AGCGGCTGGTACGCTGCTCACTAAGGGAACCAAGGAGATGAAGCTGTCGATGCTCTCT 843

DB 1792 AGCGGCTGGTACGCTGCTCACTAAGGGAACCAAGGAGATGAAGCTGTCGATGCTCTCT 1851

QY 844 ACTTCGGGAGATCTGCTGCTCACTAAGGGAACCAAGGAGATGAAGCTGTCGATGCTCTCT 903

DB 1852 ACTTCGGGAGATCTGCTGCTCACTAAGGGAACCAAGGAGATGAAGCTGTCGATGCTCTCT 1911

QY 904 CCTACTCGGCTCTTATTCGCTGAGCGTGGAGCAACTTCAACGAGGTGCTGGAGGAGTACC 963

DB 1912 CCTACTCGGCTCTTATTCGCTGAGCGTGGAGCAACTTCAACGAGGTGCTGGAGGAGTACC 1971

QY 964 CCATGATCGGGCGGCTCTTCAGAGCGTGGGATCGAGCGCTGACCGCTGACCGCATCGGCA 1023

DB 1972 CCATGATCGGGCGGCTCTTCGAGACGCTGGCCATCGACCGCTGACCGCATCGGCA 2031

QY 1024 AGAATTCATCTCTCTGACCAAGTGCAGATGACCTCAACTCGGGCTGATTTCAACAACC 1083

DB 2032 AGAATTCATCTCTCTGACCAAGTGCAGATGACCTCAACTCGGGCTGATTTCAACAACC 2091

QY 1084 AGGAGAACGCCATCATCCAGGAGATCGTCAAGTACGACCGCGAGATGGTGCAGCAGCGG 1143

DB 2092 AGGAGAACGCCATCATCCAGGAGATCGTCAAGTACGACCGCGAGATGGTGCAGCAGCGG 2151

QY 1144 AGTGGGCTCAGCGGCTGGGCTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1202

DB 2152 AGTGGG-TCAGCGGCTGGGCTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2210

QY 1203 GCCATCGCCAGCTGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1261

DB 2211 GCCATCGCCAGCTGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2270

QY 1262 CTGCTGGGCGCGCTGGGCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1321

DB 2271 CTGCTGGGCGCGCTGGGCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2330

QY 1322 GCACCTGCHGCNCTCACCC 1342

DB 2331 GCACCTGCGCGCTCACCC 2351

RESULT 4

AAD29756

ID AAD29756 standard; DNA; 3459 BP.

XX

AC AAD29756;

XX	17-MAY-2002 (first entry)	
DT	Human hyperpolarisation-activated cyclic nucleotide-gated channel 2 DNA.	
DE	Human; hyperpolarisation-activated cyclic nucleotide-gated channel; HCN;	
XX	therapy; stroke; ischaemia; head injury; epilepsy; Alzheimer's disease;	
KW	Parkinson's disease; learning disorder; memory; attention disorder; pain;	
KW	gut disorder; irritable bowel syndrome; IBS; sleep disorder; nootropic;	
KW	neuroprotective; cerebrotrophic; antiinflammatory; anticonvulsant;	
KW	tranquilliser; vasotropic; ds.	
OS	Homo sapiens.	
XX		
FH	Key Location/Qualifiers	
FT	54..2723	
FT	/*tag= a	
FT	/product= "Human HCN2 protein"	
FT		
PD	WO20020630-A2.	
XX		
PD	10-JAN-2002.	
XX		
PF	03-JUL-2001; 2001WO-GB002959.	
PR	03-JUL-2000; 2000GB-00016360.	
PR	03-NOV-2000; 2000GB-00026946.	
XX	(SMIK ) SMITHKLINE BEECHAM PLC.	
PA		
XX	Strijbos PJLM, Bates S, Gloger I, Davies C;	
PI	WPI; 2002-188422/24.	
XX	P-PSDB; AAE18676.	
DR	New HCN channel polypeptides and polynucleotides which encode the	
XX	polypeptides, for the manufacture of compositions to treat stroke,	
PT	ischemia, head injury, epilepsy, Alzheimer's disease, Parkinson's	
PT	disease.	
XX		
XX	Claim 7; Page 52-53; 68pp; English.	
XX	The invention relates to new uses of human hyperpolarisation-activated,	
CC	cyclic nucleotide-gated (HCN) channel polypeptides and their	
CC	polynucleotides. The HCN channel polypeptides and polynucleotides can be	
CC	used in the manufacture of medicaments to treat stroke, ischaemia, head	
CC	injury, epilepsy, Alzheimer's disease, Parkinson's disease, learning or	
CC	memory and attention disorders. These compounds may also be used in	
CC	treating pain, gut disorders, in particular irritable bowel syndrome	
CC	(IBS) or sleep disorders. HCN polynucleotides and polypeptides may also	
CC	be employed as diagnostic reagents for detection of mutations in the	
CC	above stated diseases. The present sequence is human HCN2 channel DNA	
XX		
SQ	Sequence 3459 BP; 569 A; 1317 C; 1094 G; 479 T; 0 U; 0 Other;	
	Query Match 96.5%; Score 1295.4; DB 6; Length 3459;	
	Best Local Similarity 99.0%; Pred. No. 5.4e-222;	
	Matches 1327; Conservative 7; Mismatches 4; Indels 3; Gaps 3;	
QY	4 TGCGCTTACCAAGATCCTCAGGCTCTGGCGGTCTGCCTTCACGCCGTGATCGGCT 63	
Dd	1030 TGCGCTTACCAAGATCCTCAGGCTCTGGCGGTCTGCCTTCACGCCGTGATCGCT 1089	
QY	64 ACATCCATCAGTGGGAGGAGATCTTCCCATGACCTATGACCTGGCCAGCGGTGATGA 123	
Dd	1090 ACATCCATCAGTGGGAGGAGATCTTCCCATGACCTATGACCTGGCCAGCGGTGATGA 1149	
QY	124 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCACCTGAGCGGCTGTCAGT 183	
Dd	1150 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCACCTGAGCGGCTGTCAGT 1209	
QY	184 TCCTGTGCCCAGTGCTGAGGACTTCCCGCGCAAAGTCTGGGTGTTCATCAATGGCATGG 243	





Db 1619 AGGAGAAAGCCATCATCAGGAGATGCTCAAGTACGACCGCGAGATGCTGCAGCAGCCG 1678

Qy 1144 AGCTGGCTCAGCGCTGGGCTCTTCCCGCGCAACTGCTGGGTGTCATCAATGGCATCG 1202

Db 1679 AGCTGGG-TAGGCGCTGGGCTTTTCCCGCGCCCGCCCGCGGAGGTCACCTTCG 1737

Qy 1203 GCCATGCCACAGCTGCAGCAGCGCGGCGGCATGAGCTTCTGCCCGCAG 1250

Db 1738 GCCATGCCACAGCTGCAGCAGCGCGGCGGCATGAGCTTCTGCCCGCAG 1785

RESULT 6

AD87558

ID ADC87558 standard; DNA; 2125 BP.

XX

AC ADC87558;

XX

DT 01-JAN-2004 (first entry)

XX

DE Human GPCR gene SEQ ID NO:2011.

XX

db; gene; human; GPCR;

KW guanosine triphosphate-binding protein coupled receptor; gene therapy.

XX

OS Homo sapiens.

XX

FN BP1270724-A2.

XX

PD 02-JAN-2003.

XX

PF 18-JUN-2002; 2002BP-00013517.

XX

PR 18-JUN-2001; 2001JP-00246789.

XX

PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

XX

PI Suwa M, Asai K, Akiyama Y, Aburatani H;

XX

DR WPI; 2003-315783/31.

DR P-PSDB; ADC87559.

XX

PT New polynucleotide, useful for preparing a composition for treating a

PT patient in need of increased or suppressed activity or expression of the

PT guanosine triphosphate-binding protein coupled receptor.

XX

PS Claim 1; SEQ ID NO 2011; 28pp; English.

XX

CC The invention relates to a novel polynucleotide encoding a guanosine

CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of

CC the invention may have a use in gene therapy. The polynucleotide and

CC polypeptide are useful for preparing a composition for treating a patient

CC in need of increased or suppressed activity or expression of the

CC guanosine triphosphate-binding protein coupled receptor. The

CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the

CC invention.

XX

SQ Sequence 2125 BP; 370 A; 721 C; 655 G; 379 T; 0 U; 0 Other;

Query Match 88.8%; Score 1191.6; DB 10; Length 2125;

Best Local Similarity 95.2%; Pred. No. 1.8e-203;

Matches 1276; Conservative 7; Mismatches 47; Indels 10; Gaps 5;

Qy 4 TGGCGTTTCAACAGATCCTCAGCCTCTCGGGCTGTGCGCTCTCAAGCTGATCGCT 63

Db 688 TGGCGTTTCAACAGATCCTCAGCCTCTCGGGCTGTGCGCTCTCGGGCTGATCGCT 747

Qy 64 ACATCCATCAGTGGAGAGATCTTCCATGACCTATGACCTGGCGCGCGGTGATGA 123

Db 748 ACATCCACCACTGGAGGAGATCTTCCATGACCTATGACCTGGCGCGCGGTGATGC 807

Qy 124 GGATCTGCATCTCATCAGATGATGCTGTGCTTGCCTGCGAGCGGTGCTGCAGT 183

Db 808 GGTCTTGCAACCTCATCAGTATGATGCTGCTGCTCTGCACTGGGATGGCTGCTGCAGT 867

Qy 184 TCTGCTGCTCCATGCTGCAGGACTTCCCGCGCAACTGCTGGGTGTCATCAATGGCATCG 243

Db 868 TCTGCTGGCCATGCTGCAGGACTTCCCGTCAACTGCTGGGTGTCATCAATGGCATGG 927

Qy 244 TGAAACACTGTGTGGAGTGAATGTGTAATCTTCCGCACTCTTCAAGGCCATGAGCCATGC 303

Db 928 TGAAACACTGTGTGGAGCGAACTGTATTTCTTCCGCACTCTTCAAGGCCATGAGCCATGC 987

Qy 304 TGTGCTATCGGCTACGCGCGGCGGCGGAGAGATGACGACATCTGGCTGACCATGC 363

Db 988 TGTGCTATCGGCTATGCGCGCGGCGGCGGAGAGATGACGACATCTGGCTGACCATGC 1047

Qy 364 TCAGCATGATTTGCTGGTGCACCTGCTAGCCATGTTTATCGGCCCAACGCTGACCTCA 423

Db 1048 TCAGCATGATTTGCTGGTGCACCTGCTAGCCATGTTTATCGGCCCAACGCTGACCTCA 1107

Qy 424 TCCAGTTCGCTGACTCTCGCGCGCCAGTACAGAGAAAGTACAGAGAGTGGAGCAGT 483

Db 1108 TCCAGTTCGCTGACTCTCGCGCGCCAAATAC--AGAAAGTACAGAGAGTGGAGCAGT 1164

Qy 484 ACATGCTCTTCCAAAGCTGCGAGTCTCGCCGAGAGATCCACGACTACTATGAGC 543

Db 1165 ACATGCTCTTCCAAAGCTGCGCGCGGACTTCCCGCAGAAAGATCCACGACTACTACGAGC 1224

Qy 544 ACCGTTACCAGGCGCAAGATGTTTTCAGAGGACAGATCTCGCGCGAGCTCAACGGGCCCC 603

Db 1225 ACCGTTACCAGGCGCAAGATGTTTTCAGAGGACAGATCTCGCGCGAGCTCAACGGGCCCC 1284

Qy 604 TCGCGGAGGAGATCGTCAACTTCAACTGCGGAAAGCTGCTGACCTCCATCGCGCTGTTG 663

Db 1285 TCGCGGAGGAGATGTTCAACTTCAACTGCGGAAAGCTGCTGACCTCCATCGCGCTGTTG 1344

Qy 664 CCAGCGCGACCCCAACTTCTGTCAGCGCATGCTGACCAAGCTCAAGTTCGAGGCTTCC 723

Db 1345 CCAATGCTGACCCCAACTTCTGTCAGCGCATGCTGACCAAGCTCAAGTTCGAGGCTTCC 1404

Qy 724 AGCGGGTCACTACATCATCCGGAAGGACCATCCGGAAGAGATGTACTTTCATCCAGC 783

Db 1405 AGCGGGTCACTACATCATCCGGAAGGACCATCCGGAAGGACCATCCG--GAAGATGTACTTTCATCCAGC 1461

Qy 784 AGCGGTGTGTGAGCGTGTCTACTAAGGGCAACAGAGAGATGAAGTGTCCGATGGCTCTCT 843

Db 1462 AGCGGTGTGTGAGCGTGTCTACTAAGGGCAACAGAGAGATGAAGTGTTCGATGGCTCTCT 1521

Qy 844 ACTTCGGGAGATCTGCTGCTCAACCGGGGGCGCGCAGCGGAGCGTGCAGGCTGACA 903

Db 1522 ACTTCGGGAGATCTGCTGCTCAACCGGGGGCGCGCAGCGGAGCGTGCAGGCTGACA 1581

Qy 904 CCTACTGCGCGCTCTATTTCGCTGAGGTGAGCAACTTCAACGAGGTGCTGGAGAGTACC 963

Db 1582 CCTATTGCGCGCTCTTTCGCTGAGGTGAGCAACTTCAACGAGGTGCTGGAGAGTACC 1641

Qy 964 CCATGATGCGGGCGCGCTTTCGAGAGCGTGGCCATCGACCGCTTGGAGCGCATCGGCAAGA 1023

Db 1642 CCATGATGCGGGCGCGCTTTCGAGAGCGTGGCCATCGACCGCTTGGAGCGCATCGGCAAGA 1701

Qy 1024 AGAATTCATCTCTGCAAGGTCAGCATGACCTCAACTCGGGCGGTATTCAACNACC 1083

Db 1702 AGAATTCATCTCTCTGCAAGGTCAGCATGACCTTAACTCGGGCGGTATTCAACNACC 1761

Qy 1084 AGGAGAACGCCATCATCCAGGAGATGCTCAAGTACGACCGCGAGATGTTGACAGCGCG 1143

Db 1762 AGTAGAACGCCATCATCCAGGAGATGCTCAAGTACGACCGCGAGATGTTGACAGCGCG 1821

Qy 1144 AGCTGGGCTCAGCGCTGGGCGCTCTTTCGCGCGCGCGCGCGCGCGCGCGAGTCACTCGG 1203

Db 1822 AGCTGGG-TCAGGCGCTTGGCGCTCTTCCGCGCGCGCGCGCGCGAG--GTCACTCTCG 1878

Qy 1204 CCATCGCCACGCTGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1262

Db 1879 CCATCGCCACGCTGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1938

QY 1263 TCGTGGGGCGCTGGCGCTCGGCTCGCGCGCTCGTGGCHGCHYNDYHCCCGGSGCG 1322  
Db 1939 TCGTGGGGCGCTGGCGCTCGGCTCGCGCGCTCGTGGCGCGCGCGCGCGCGCG 1998  
QY 1323 CACCTGCHGCGNCTCACCC 1342  
Db 1999 CACCTGCGCGCGCTCACCC 2018

RESULT 7  
AAH98302  
ID AAH98302 standard; cDNA; 3431 BP.  
XX AAH98302;  
AC  
XX  
DT 12-OCT-2001 (first entry)  
XX Human EST-derived coding sequence SEQ ID NO: 159.  
DE  
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;  
KW gene therapy; nutrition; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200154477-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001WO-US002687.  
XX  
PR 25-JAN-2000; 2000US-00491404.  
PR 17-JUL-2000; 2000US-00617746.  
PR 03-AUG-2000; 2000US-00631451.  
PR 15-SEP-2000; 2000US-00663870.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
XX  
XX WPI: 2001-476164/51.  
DR P-PSDB; AAM23643.  
XX  
PT Isolated polypeptide for treatment of diseases, diagnostics, raising  
PT antibodies and research use.  
XX  
PS Claim 1; Page 282-283; 1275pp; English.  
XX  
CC The present invention provides the protein and coding sequences of novel  
CC proteins from a variety of organisms, including human, dog, cat, horse,  
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
CC from the organism of interest. They can be used in diagnostics,  
CC forensics, gene mapping, identification of mutations, to assess  
CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
CC of the invention  
XX  
SQ Sequence 3431 BP; 524 A; 1312 C; 1105 G; 490 T; 0 U; 0 Other;

Query Match 83.0%; Score 1113.2; DB 4; Length 3431;  
Best Local Similarity 93.2%; Pred. No. 1.8e-189;  
Matches 1270; Conservative 7; Mismatches 61; Indels 24; Gaps 10;

QY 4 TCGCGTTACCAAGATCCCTCAGCCTCTCGGCTCGGCTCTCAGCCCTGATCCGCT 63  
Db 1030 TCGCGTTACCAAGATCCCTCAGCCTCTCGGCTCGGCTCTCAGCCCTGATCCGCT 1089  
QY 64 ACATCATCAGTGGGAGAGATCTTCCACATGACCTATGACCTGGCGAGCGGTGATGA 123  
Db 1090 ACATCATCAGTGGGAGAGATCTTCCACATGACCTATGACCTGGCGAGCGGTGATGA 1149

QY 124 GGATCTGCAATCTCATCAGCATGATGCTGCTGCTGCTGCACTGGGACGCGCTGCGCTGCACT 183  
Db 1150 GGATCTGCAATCTCATCAGCATGATGCTGCTGCTGCTGCACTGGGACGCGCTGCGCTGCACT 1209  
QY 184 TCCTGGTGGCCATGCTGAGGACTTCCCGCGCAACTGCTGGGTGCTCCATCAATGGCATGG 243  
Db 1210 TCCTGGTGGCCATGCTGAGGACTTCCCGCGCAACTGCTGGGTGCTCCATCAATGGCATGG 1269  
QY 244 TGAACCACTCGTGGAGTGAATGTTACTCTTTCGCACTTTCAAGGCCATAGGCCACATGC 303  
Db 1270 TGAACCACTCGTGGAGTGAATGTTACTCTTTCGCACTTTCAAGGCCATAGGCCACATGC 1329  
QY 304 TGTGCATCGGTACGGCCGGCAGGCGCGGAGAGATGACGACATCTGGCTGACCATGC 363  
Db 1330 TGTGCATCGGTACGGCCGGCAGGCGCGGAGAGATGACGACATCTGGCTGACCATGC 1389  
QY 364 TCAGCATGATTTGGGTGCCACTCTGCTACGCCATGTTTCATCGGCCACGCCACTGCGCTCA 423  
Db 1390 TCAGCATGATTTGGGTGCCACTCTGCTACGCCATGTTTCATCGGCCACGCCACTGCGCTCA 1449  
QY 424 TCCAGTCTGCTGACTCTCTCGCGGCCAGTACCAGGAGAGTACAGGAGGTGGAGCACT 483  
Db 1450 TCCAGTCTGCTGACTCTCTCGCGGCCAGTACCAGGAGAGTACAGGAGGTGGAGCACT 1509  
QY 484 ACATGTCCTTCCACAAAGCTGCCAGTACTTCCGCGAGAGATCCACGACTACTATGAGC 543  
Db 1510 ACATGTCCTTCCACAAAGCTGCCAGTACTTCCGCGAGAGATCCACGACTACTATGAGC 1569  
QY 544 ACCGTTACAGGGCAAGATGTTTACGAGGAGCAGCATCTTGGGCGAGCTCAACGGGCCCC 603  
Db 1570 ACCGTTACAGGGCAAGATGTTTACGAGGAGCAGCATCTTGGGCGAGCTCAACGGGCCCC 1629  
QY 604 TCGCGGAGGAGATCGTCAACTTCAATCCCGGAGCTGGTGGCTTCCATGCGCTGTTGC 663  
Db 1630 TCGCGGAGGAGATCGTCAACTTCAATCCCGGAGCTGGTGGCTTCCATGCGCTGTTGC 1689  
QY 664 CCAAGCCGACCCCAACTTCTGTCAGGCGCATGCTGACCAAGCTCAAGTTCGAGGCTTCCC 723  
Db 1690 CCAAGCCGACCCCAACTTCTGTCAGGCGCATGCTGACCAAGCTCAAGTTCGAGGCTTCCC 1749  
QY 724 AGCGGGTGACTACATCAT - CGCGAAGGACCATCGGGAAGAGATGTACTTCAATCCAG 782  
Db 1750 AGCGGGTGACTACATCATCGCGAAGGACCATCGGGAAGAGATGTACTTCAATCCAG 1809  
QY 783 CACGCGTGGTCAGCGTCTCACTAAGGGCAACAGGAGATGAAGCTGTCGATGGCTCC 842  
Db 1810 CACGCGTGGTCAGCGTCTCACTAAGGGCAACAGGAGATGAAGCTGTCGATGGCTCC 1869  
QY 843 TACTTCGGGAGATCTGCTGCTCAACCGGGGCGCGCAGCGGAGCGTGGCGGCTGAC 902  
Db 1870 TACTTCGGGAGATCTGCTGCTCAACCGGGGCGCGCAGCGGAGCGTGGCGGCTGAC 1929  
QY 903 ACCTACT-----GCCGCTCTATTTCGCTGAGCGTGGACAACCTTCAACGAGGTGCT---- 952  
Db 1930 ACAACCTTATTTCGCGGCTCTTATTTCGCTGAGCGTGGACAACCTTCAACGAGGTGCTTGA 1989  
QY 953 GGAGGAGTACCCCATGATTCGCGCGCGCTTCGAGACGCTGGGCCAT - CGACCGCTGGAC 1010  
Db 1990 GGAGTAAACCCCATGATTCGCGGCGCTTCGAGACGCTTCGAAACCGCTGGAC 2049  
QY 1011 CGCA--TCGGCAAGAGAAATTCATCC--TCTGCAAGGTGGAGCATGACCTCAATC 1066  
Db 2050 CGCATTTTCGGAAGAAAGAAATTCATTCCTGCTGCAAGGTGGAGCATGACCTCAATC 2109  
QY 1067 GGGCGTATTCAACAAACAGGAGAACGCCATCATCCAGGAGATCGTCAAGTAGACGCGCA 1126  
Db 2110 GGGCGTATTCAACAAACAGGAGAACGCCATCATCCAGGAGATCGTCAAGTAGACGCGCA 2169  
QY 1127 GATGTCAGAGCGCGGAGCTGGGTTCAGCGGTGGGCTCTT - CCGCGCGCGCGCGCG 1185  
Db 2170 GATGTCAGAGCGCGGAGCTGGG - TCAGCGGTGGGCTCTTACCCGCGCGCGCGCGCG 2228





Db 1583 GAACCTCGATCTGCTACACAGGTGTCAGCACGACCTCAACTCTGGCGTGTAAACACCA 1642  
Qy 1085 GGAGAACCCATCATCCAGGAGATCGTCAAGTACGACCGGAGATGTGACAGAGGCCGA 1144  
Db 1643 GGAGAACCCATCATCCAGGAGATGTCAAGTATGACCGGAGATGTGACAGAGGTGA 1702  
Qy 1145 GCTGGGCTCAGCGGTGGGCTCTTCCGCGCGCGCGCGCGCGCGCA-GTCACTCTCG 1203  
Db 1703 GCTGGGC-CAGCGTGTGGCTCTTCCGCGCACCGCCACCTCCACAGGCACTCAG 1761  
Qy 1204 CCATCGCCACGCTCAGAGAGCGCGGCGCATGAGCTTCTGCGCGCA 1249  
Db 1762 CCATTGCCACGCTCAGCA-GCCGTGGCCATGAGCTTCTGTCCACA 1806

RESULT 10

AAZ09491  
ID AAZ09491 standard; DNA; 2886 BP.

AC AAZ09491;

DT 02-NOV-1999 (first entry)

XX Human Ih ion channel DNA fragment #2.

XX Ih ion channel; human; sea urchin; fruit fly; rat; bovine; analgesic;  
KW cardioactive; pacemaker; cardiac muscle; ion channel modulator;  
KW treatment; diagnosis; ion channel-related disease; cardiac disease;  
KW circulatory disorder; sinus ganglion regulation; sleep disorder;  
KW cortico-thalamic neuron; pain; detection; mutation; ss.

XX Homo sapiens.

XX WO9942574-A1.

XX 26-AUG-1999.

XX 12-FEB-1999; 99WO-EP000942.

XX 17-FEB-1998; 98DE-01006581.

XX (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.

XX Baumann A, Boenigk W, Gauss R, Scholten A, Seifert R, Kaupp B;

XX WPI; 1999-527472/44.

XX New nucleic acid encoding an Ih ion channel, used to identify specific  
PT modulators, and for treatment, prevention and diagnosis of e.g. cardiac  
PT disease.

XX Disclosure; Page 67-68; 82pp; German.

XX This invention describes a novel Ih ion channel, isolated from human, sea  
CC urchin, bovine, rat, and fruitfly. The ion channels of the invention have  
CC analgesic and cardioactive activity. The Ih ion channel participates in  
CC the pacemaker function in cardiac muscle. The Ih ion channel nucleic acid  
CC and its encoding protein is used to identify substances (A) that modulate  
CC activity of ion channels; to treat and/or diagnose ion channel-related  
CC diseases, particularly cardiac or circulatory disorders and to prevent  
CC and/or treat cardiac/circulatory disorders (especially faulty regulation  
CC of the sinus ganglion), sleep disorders (particularly abnormal function  
CC of cortico-thalamic neurons) and/or pain. Fragments of the Ih ion channel  
CC nucleic acid are used to detect mutations e.g. for differential  
CC diagnosis. This sequence encodes a human Ih channel fragment isolated  
CC from human thalamus tissue

XX Sequence 2886 BP; 605 A; 774 C; 940 G; 558 T; 0 U; 9 Other;

Query Match 73.9%; Score 992.4; DB 2; Length 2886;

Best Local Similarity 98.8%; Pred. No. 6.4e-168;

Matches 1007; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

RESULT 11

AAZ09496

ID AAZ09496 standard; DNA; 4751 BP.

XX

Qy 4 TGGCGTTCCACCAAGATTCCTCAGCCTCTCTGGGGTGTGGCGCTCTCAGCGCTGATCGGCT 63  
Db 521 TGGCGTTCCACCAAGATTCCTCAGCCTCTCTGGGGTGTGGCGCTCTCAGCGCTGATCGGCT 580  
Qy 64 ACATCCATCAGTGGGAGGAGATCTTCACATGACCTATGACCTGGGCGAGCGGCTGATGA 123  
Db 581 ACATCCATCAGTGGGAGGAGATCTTCACATGACCTATGACCTGGGCGAGCGGCTGATGA 640  
Qy 124 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCACTGGGAGCGGCTGCTGCACT 183  
Db 641 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCACTGGGAGCGGCTGCTGCACT 700  
Qy 184 TCTGCTGGCCATGCTGTCAGGACTTCCCGCGCAACTGCTGGGGTGTCAATCAATGGCATGG 243  
Db 701 TCTGCTGGCCATGCTGTCAGGACTTCCCGCGCAACTGCTGGGGTGTCAATCAATGGCATGG 760  
Qy 244 TGAACCACTCGTGGAGTGAATGTAATCTCTTGGCACTCTTCAAGGCCATGAGCCATGTC 303  
Db 761 TGAACCACTCGTGGAGTGAATGTAATCTCTTGGCACTCTTCAAGGCCATGAGCCATGTC 820  
Qy 304 TGTGATCGGTTACGCGCGGAGGCGCGGAGAGCATGACGGACATCTGCTGACCATGTC 363  
Db 821 TGTGATCGGTTACGCGCGGAGGCGCGGAGAGCATGACGGACATCTGCTGACCATGTC 880  
Qy 364 TCAGCATGATGTTGGTGGCCACTGCTAGCCCATGTTCAATGGCCACGCCACTGCCCCCTCA 423  
Db 881 TCAGCATGATGTTGGTGGCCACTGCTAGCCCATGTTCAATGGCCACGCCACTGCCCCCTCA 940  
Qy 424 TCCAGTCTGGACTCTCTCGCGCGCAGTACCAAGAGAGTACCAAGAGGTTGGAGCAGT 483  
Db 941 TCCAGTCTGGACTCTCTCGCGCGCAGTACCAAGAGAGTACCAAGAGGTTGGAGCAGT 1000  
Qy 484 ACATGTCCTTCCAAAGCTGCGAGTGAATCTTCGCGCAGAAAGATCCACAGCTACTATGAGC 543  
Db 1001 ACATGTCCTTCCAAAGCTGCGAGTGAATCTTCGCGCAGAAAGATCCACAGCTACTATGAGC 1060  
Qy 544 ACCGTTTACCAGGGCAAGATGTTTTCAGGAGACAGCATCTTGGCGAGCTCAACGGGCCCC 603  
Db 1061 ACCGTTTACCAGGGCAAGATGTTTTCAGGAGACAGCATCTTGGCGAGCTCAACGGGCGCN 1120  
Qy 604 TGGCGGAGGAGATCGTCAACTTCACTGCGGAGAGCTGTTGGCTCGATCCGCTGTTTCG 663  
Db 1121 TGGCGNAGGAGATCGTCAACTTCACTGCGGAGAGCTGTTGGCTCGATCCGCTGTTTCG 1180  
Qy 664 CCAGCCCGGACCCCAACTTCTGTCACGCGCATCTGACCAAGCTCAAGTTTCGAGGCTTCTTC 723  
Db 1181 CCAGCCCGGACCCCAACTTCTGTCACGCGCATCTGACCAAGCTCAAGTTTCGAGGCTTCTTC 1240  
Qy 724 AGCGGGTGACTACATCATCCGGAAGGACCATCCGGAAGAGATGTACTTTCATCCAGC 783  
Db 1241 AGCGGGTGACTACATCATCCGGAAGGACCATCCGGAAGAGATGTACTTTCATCCAGC 1300  
Qy 784 AGCGGGTGACTAGCGTGAATCACTAAGGGCAACAAAGAGATGAAGCTGTCGATGGCTCTCT 843  
Db 1301 AGCGGGTGACTAGCGTGAATCACTAAGGGCAACAAAGAGATGAAGCTGTCGATGGCTCTCT 1360  
Qy 844 ACTTGGGAGAGATGCTGCTGCTCACCGGGGCGCGCAGCGGAGCTGCGGGCTGACA 903  
Db 1361 ACTTGGGAGAGATGCTGCTGCTCACCGGGGCGCGCAGCGGAGCTGCGGGCTGACA 1419  
Qy 904 CCTACTGCGCGCTCTATTTCGCTGAGCGTGGCAAACTTCAACGAGGTTGCTGGAGAGTACC 963  
Db 1420 CCTACTGCGCGCTCTATTTCGCTGAGCGTGGCAAACTTCAACGAGTGTGGAGAGTACC 1479  
Qy 964 CCATGATGCGGCGCGCTTTCGAGACGCGTGGCCATCGACCGCTGGACCGCATCGGCAG 1022  
Db 1480 CCATGATGCGGCGCGCTTTCGAGACGCGTGGCCATCGACCGCTGGACCGCATCGGTGAG 1538





XX DE Human hyperpolarisation-activated cyclic nucleotide-gated channel 4 DNA.

XX KW Human; hyperpolarisation-activated cyclic nucleotide-gated channel; HCN; therapy; stroke; ischaemia; head injury; epilepsy; Alzheimer's disease; Parkinson's disease; learning disorder; memory; attention disorder; pain; gut disorder; irritable bowel syndrome; IBS; sleep disorder; nootropic; neuroprotective; cerebroprotective; antiinflammatory; anticonvulsant; tranquiliser; vasotropic; ds.

XX KW Homo sapiens.

XX OS

XX PH Key Location/Qualifiers

XX FT CDS 997..4608

XX FT /\*cag= a

XX FT /product= "Human HCN4 protein"

XX PN W0200202630-A2.

XX PD 10-JAN-2002.

XX PF 03-JUL-2001; 2001WO-GB002959.

XX PR 03-JUL-2000; 2000GB-00016360.

XX PR 03-NOV-2000; 2000GB-00026946.

XX XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX PA Strijbos PJLM, Bates S, Gloger I, Davies C;

XX PI WPI; 2002-188422/24.

XX DR P-PSDB; AAE18677.

XX XX New HCN channel polypeptides and polynucleotides which encode the polypeptides, for the manufacture of compositions to treat stroke, ischemia, head injury, epilepsy, Alzheimer's disease, Parkinson's disease.

XX PS Claim 7; Page 55-57; 68pp; English.

XX XX The invention relates to new uses of human hyperpolarisation-activated, cyclic nucleotide-gated (HCN) channel polypeptides and their polynucleotides. The HCN channel polypeptides and polynucleotides can be used in the manufacture of medicaments to treat stroke, ischaemia, head injury, epilepsy, Alzheimer's disease, Parkinson's disease, learning or memory and attention disorders. These compounds may also be used in treating pain, gut disorders, in particular irritable bowel syndrome (IBS) or sleep disorders. HCN polynucleotides and polypeptides may also be employed as diagnostic reagents for detection of mutations in the above stated diseases. The present sequence is human HCN4 channel DNA

XX SQ Sequence 4751 BP; 828 A; 1737 C; 1427 G; 759 T; 0 U; 0 Other;

Query Match 69.1%; Score 927.2; DB 6; Length 4751;

Best Local Similarity 84.7%; Pred. No. 2.9e-156;

Matches 1040; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 4 TCGCGTTCCACCAAGATCTCAGCCTCTCGCGGCTGCTCGCCTCTCAGCCTGATCCGCT 63

DB 2126 TCCGCTTCCAGAGATCTCAGCCTCTTACGCTGTTAGCCTCTCCGCGCTCATTCGAT 2185

QY 64 ACATCATCAGTGGAGAGATCTTCCACATGACCTATGACCTGGCCAGCGCGGTGATGA 123

DB 2186 ATATTCACAGTGGGAAGAGATCTTCCACATGACCTAGACCTGGCCAGCGCGGTGTC 2245

QY 124 GGATCTGAATCTATCAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183

DB 2246 GCATCGTGAACCTCATCGGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2305

QY 184 TCCTGGTGGCCATGCTGAGGAGATTTCCCGCGCAACTGCTGGGTGTTCATCAATGGCATGG 243

DB 2306 TCCTGGTACCACATGCTACAGGACTTCCCTGACGACTGCTGGGTGTTCATCAACACATGG 2365

QY 244 TGAACCACTCTGTGGAGTGAATGTACTCTTCGCACTCTTTCAAGGCCATGAGCCATGCG 303

DB 2366 TGAACCACTCTCTGGGGAAGCAGTACTCTTACGCGCTCTTCAAGGCCATGAGCCATGCG 2425

QY 304 TGTGCATCGGTTACGGCCGGCAGGCGCCGAGAGCATGACGACATCTCGCTGACCATGCG 363

DB 2426 TGTGCATCGGCTACGGCGGCGAGGCGCCGCTGGGCGATGTCGACGCTCTGGCTCACCATGCG 2485

QY 364 TCAGCATGATTTGGGTGCCACTGCTAGCGCATGTTTCATCGGCCACGCGCACTGCGCTCA 423

DB 2486 TCAGCATGATCGTGGGTGCCACTGCTAGCGCATGTTTCATCGGCCACGCGCACTGCGCTCA 2545

QY 424 TCCAGTCTGTGACTCTCTCGCGCGCCAGTACAGAGAGAAATACAGAGAGGTGGAGCAGT 483

DB 2546 TCCAGTCTCTGACTCTCTCGCGCGCCAGTACAGAGAGAAATACAGAGAGGTGGAGCAGT 2605

QY 484 ACATGTCCTTCCACAAGCTGCCAGCTGACTTCCGCCAGAGATCCACAGACTACTATGAGC 543

DB 2606 ACATGTCCTTCCACAAGCTGCCCGCCGACACCGCGCAGCGCATCCACAGACTACTATGAGC 2665

QY 544 ACCGTTTACCAGGGAAGATGTTTGACGAGCAGCAGCATCTCTGGCGCAGAGCTCAACGGGCCCC 603

DB 2666 ACCGTTTACCAGGGAAGATGTTTGACGAGCAGCAGCATCTCTGGCGCAGAGCTAAAGCGGCC 2725

QY 604 TCGCGGAGGAGATCGTCAACTTCAACTGCCGGAAGCTGTGGCTTCCATGCCCGCTGTTG 663

DB 2726 TCGCGGAGGAGATCATCAACTTTAACTGTGGGAAGCTGTGGCTTCCATGCCCACTGTTT 2785

QY 664 CMAACGCCAGCCCAACTTCTGTCAGCGCCATGCTGACCAAGCTCAAGTTCGAGGTCTTCC 723

DB 2786 CCAATCGGAGCCCAACTTCTGTCAGCTTCCATGTCACCAAGCTGCGTTCGAGGTCTTCC 2845

QY 724 AGCGCGGTGACTATCATCTCCGGAAGGCAACCATCGGGAAGAGATGTACTTTCATCCAGC 783

DB 2846 AGCGTGGGACTATCATCTCCGGAAGGCAACCATTCGCAAGAGATGTACTTTCATCCAGC 2905

QY 784 ACGGCTGTGTGACGCTGCTCACTAAGGGCAACAGGAGATGAAGCTGTTCGATGGCTCT 843

DB 2906 ATGGCGTGTGTGACGCTGCTCACTAAGGGCAACAGGAGATGAAGCTGTTCGATGGCTCT 2965

QY 844 ACTTCGGGAGATCTGCTGCTCACTCCCGGGCGCCGCGCAGCGGCGTGGCGGTGACCA 903

DB 2966 ACTTTGGAGAGATCTGCTGCTGACCCCGGGCGCCGCGCAGCGGTGAGGCGCCGACCA 3025

QY 904 CCTACTGCGCGCTCTATTGCTGAGCGTGGACAACATTTCAACGAGGTGCTGGAGAGTACC 963

DB 3026 CCTACTGCGCGCTCTATTGCTGAGCGTGGACAACATTTCAATGAGGTGCTGGAGAGTACC 3085

QY 964 CCATGATGCGCGCGCTTTTCGAGACGCTGGCCCATTCGACCGCTGGACCGCATCGGCAAGA 1023

DB 3086 CCATGATGCGAAGGGCTTTCGAGACCGTGGCGCTGGACCGCTGGACCGCATTTGGCAAGA 3145

QY 1024 AGAATTCATCTCTTCGCAAGGTGAGCATGACCTCAACTCGGGGGTATTCAACNACC 1083

DB 3146 AGAATTCATCTCTCTCCACAAAGTCCAGCACACCTCAACTCCGCGCTTTCAACTACC 3205

QY 1084 AGAGAACGCAATCATTCAGAGATGCTCAAGTACGACCGCGAGATGGTGCAGCAGCGCG 1143

DB 3206 AGGAGATGAGATCATCTCCAGCAGATTTGTGAGCATGACCGGGAGATGGCCCATCTGCGCGC 3265

QY 1144 AGCTGGGCTCAGCGCGTGGGCTCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1203

DB 3266 ACCGCTGTCAGGCTGTGCTCTTGCCACCCCAACCCCAACCCCAACCCCAACCCCAACCC 3325

QY 1204 CCATCGCCACGCTGTCAGCAGCGCGCGCG 1231

DB 3326 TGATCCAGGACCACTGCGAGGCTGCGCG 3353

RESULT 13  
AAH48730  
ID AAH48730 standard; cDNA; 5065 BP.  
XX

AC AAH48730;  
XX 26-OCT-2001 (first entry)  
XX Human HCN4 cDNA.  
DE Human; activator; patch-clamp; high through-put screening; inhibitor;  
KW hyperpolarization-activated cation channel; HCN4; ss.  
XX Homo sapiens.  
XX OS  
XX PH Location/Qualifiers  
XX CDS 587..4178  
XX FT /\*tag= a  
XX FT /product= "HCN4"  
XX WO200159153-A2.  
XX 16-AUG-2001.  
XX 24-JAN-2001; 2001WO-EP000755.  
XX 12-FEB-2000; 2000DE-01006309.  
XX (AVET ) AVENTIS PHARMA DEUT GMBH.  
XX Jansen H, Brueggemann A, Heitsch H, Goegelein H;  
XX WPI; 2001-550023/61.  
XX P-PSDB; AAB86462.  
XX Identifying substances which modify activity of hyperpolarization-  
PT activated cation channels using fluorescent imaging is useful to identify  
PT possible therapeutic pharmaceuticals.  
XX Disclosure; Page 44-46; 58pp; German.  
XX  
XX This invention describes a novel method for identifying substances which  
CC modify activity of hyperpolarization-activated cation channels (HACC), by  
CC placing cells which express an HACC in an iso-osmotic sodium ion-free  
CC buffer in the presence of a potential-sensitive fluorescent dye, and  
CC measuring membrane potential after the addition of sodium ions. The  
CC invention is used to identify activators or inhibitors of HACCs. Unlike  
CC prior art patch-clamp techniques, this invention can be automated, and  
CC allows high through put screening. This sequence encodes the human  
CC hyperpolarization-activated cation channel protein HCN4 which is  
CC described in the method of the invention  
XX  
SQ Sequence 5065 BP; 919 A; 1783 C; 1497 G; 866 T; 0 U; 0 Other;  
  
Query Match 69.1%; Score 927.2; DB 4; Length 5065;  
Best Local Similarity 84.7%; Pred. No. 2.9e-156;  
Matches 1040; Conservative 0; Mismatches 188; Indels 0; Gaps 0;  
  
QY 4 TGGCTTACCAAGATCTCAGCCTCTGGGGTGTGGCTCTTCCGCTTCAATCGAT 63  
DB 1696 TCGGCTTCAAGATCTCAGCCTCTTACGCTGTACGCTCTCCGCTTCAATCGAT 1755  
  
QY 64 ACATCATCATGTGGAGGAGATCTCCACATGACCTTATGACCTGGCCAGCGGTGATGA 123  
DB 1756 ATATTACCAAGTGGAGAGATCTTCCATGATGACCTTACGCTGGCCAGCGGTGATG 1815  
  
QY 124 GGATCTGCAATCTCATCAGCATGATGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 183  
DB 1816 GCATGTGCAATCTCATCAGCATGATGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1875  
  
QY 184 TCTGTGTCATGCTGTCAGGACTTCCGCGCACTTACCTGCTGGGTGTCCATATGGCATGG 243  
DB 1876 TCTGTGTCATGCTGTCAGGACTTCCGCGCACTTACCTGCTGGGTGTCCATATGGCATGG 1935  
  
QY 244 TGAACCACTCGTGGAGTGAATCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 303  
DB 1936 TGAACCACTCGTGGAGGAGCACTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1995

QY 304 TGTGATCGGCTACGGCCGCGCAGCGCGCGGAGAGATGACGAGCATCTGGCTGACCATGC 363  
DB 1996 TGTGATCGGCTACGGCCGCGCAGCGCGCGGAGAGATGTCGACATCTGGCTTACCATGC 2055  
  
QY 364 TCAGCATATTGTGGGTGCCACCTGTACGCATATGTTTCATCGGCGCACGCCACTGCCTCA 423  
DB 2056 TCAGCATATTGTGGGTGCCACCTGTACGCATATGTTTCATCGGCGCACGCCACTGCCTCA 2115  
  
QY 424 TCCAGTCTGCTGCACTCTCGCGGCGCCAGTACCGAGGAGAGTACAAAGCAGGTGGAGCAGT 483  
DB 2116 TCCAGTCTGCACTCTCGCGGCGCCAGTACCGAGGAGAGTACAAAGCAGGTGGAGCAGT 2175  
  
QY 484 ACATGCTCTTCCACAGCTGTCAGTGTCTCCGCGCAGAGATCCACGACTACTATGAGC 543  
DB 2176 ACATGCTCTTCCACAGCTGTCAGTGTCTCCGCGCAGAGATCCACGACTACTATGAGC 2235  
  
QY 544 ACCGTTACAGGGCAAGATGTTTACGAGGAGCAGCATCTGGCGGAGCTCAACGGGCCCC 603  
DB 2236 ACCGTTACAGGGCAAGATGTTTACGAGGAGGAGCATCTGGCGGAGCTTACGGAGCCCC 2295  
  
QY 604 TCGCGGAGGAGATCGTCAACTTCACTCCGGAAGCTGGTGGCTTCCATGCCGCTGTTCG 663  
DB 2296 TCGCGGAGGAGATCATCAACTTCACTCCGGAAGCTGGTGGCTTCCATGCCGCTGTTCG 2355  
  
QY 664 CCAAGCCGCGCCCAACTTCTGTCAGGCGCATGCTGACCAAGCTCAAGTTCGAGGTCTTCC 723  
DB 2356 CCAAGTCGCGGACCCCAACTTCTGTCAGGCGCATGCTGACCAAGCTCAAGTTCGAGGTCTTCC 2415  
  
QY 724 AGCGGGTGTACTATCATCTCCGGAAGCAGCATCTGGGAAGAGATGTACTTTCATCCAGC 783  
DB 2416 AGCGGGTGTACTATCATCTCCGGAAGCAGCATCTGGGAAGAGATGTACTTTCATCCAGC 2475  
  
QY 784 AGCGGCTGTGTCAGCGTGTCTCACTAAGGCGCAACAGGAGATGAAGTGTCCGATGGCTCT 843  
DB 2476 ATGCGTGTGTCAGCGTGTCTCACTAAGGCGCAACAGGAGATGAAGTGTCCGATGGCTCT 2535  
  
QY 844 ACTTCGGGAGATCTGCTCTGCTCAGCGCGCGCGCGCAGCGAGCTGCGGGCTGACA 903  
DB 2536 ACTTCGGGAGATCTGCTCTGCTCAGCGCGCGCGCGCAGCGAGCTGCGGGCTGACA 2595  
  
QY 904 CCTACTCGCGCTCTATTTCGCTGAGCGTGGACAACTTCAACGAGGTGTGTGGAGGAGTACC 963  
DB 2596 CCTACTCGCGCTCTATTTCGCTGAGCGTGGACAACTTCAACGAGGTGTGTGGAGGAGTACC 2655  
  
QY 964 CCATGATCGCGCGCGCTTTCGAGACGCTGGCCATCGACCGCTTGACCGCATCGGCAAGA 1023  
DB 2656 CCATGATCGAAGGGCTTTCGAGACGCTGGCGCTGGACCGCTTGACCGCATCGGCAAGA 2715  
  
QY 1024 AGAATTCATCTCTGTCACAGGTGTCAGCATGACCTCACTCGGGCGGTATTCAACACCC 1083  
DB 2716 AGAATTCATCTCTGTCACAGGTGTCAGCATGACCTCACTCGGGCGGTATTCAACACCC 2775  
  
QY 1084 AGGAAACGCCCATCATCCAGGAGATCGTCAAGTACGACCGCGAGATGGTCAGCAGCGCG 1143  
DB 2776 AGGAAATGAGATCATCCAGCAGATGTCAGCATGACCGGAGATGGCCCACTGCGCGC 2835  
  
QY 1144 AGCTGGGCTGACGCGGTGGCGCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1203  
DB 2836 AGCGGTCGAGGCTGCTGCTCTGCGCACCCCAACCCCAACCCCAACCCCAACCCCAAC 2895  
  
QY 1204 CCATCGCCACCGTGCAGCAGCGGGCGGC 1231  
DB 2896 TGATCCAGGCACCACTGCAGGCTGCCGC 2923  
  
RESULT 14  
ADR86593  
ID ADR86593 standard; cDNA; 5065 BP.  
XX  
XX ADR86593;  
XX  
XX 02-DBC-2004 (first entry)  
DT

XX DE Human HCN4 gene.

XX KW hyperpolarisation activated cyclic nucleotide-gated potassium channel 4;

XX KW HCN4; arrhythmia inducing disease; gene therapy;

XX KW hereditary QT extension syndrome; idiopathic ventricular fibrillation;

XX KW human; gene; ss.

XX OS Homo sapiens.

XX FH Location/Qualifiers

XX FT 567..4178

XX FT CDS

XX FT /\*tag= a

XX FT /product= "Human hyperpolarisation activated cyclic

XX FT nucleotide-gated potassium channel 4 protein"

XX JP2004254628-A.

XX PN 16-SEP-2004.

XX XX 27-FEB-2003; 2003JP-00050469.

XX PF WPI; 2004-657632/64.

XX PR P-PSDB; ADR86636.

XX PA (KIMU/) KIMURA A.

XX PA Novel variant of hyperpolarization activation cyclic-nucleotide

XX PT dependence channel gene, useful for diagnosing arrhythmia inducing

XX PT disease e.g., idiopathic ventricular fibrillation.

XX PS Claim 2; SEQ ID NO 1; 35pp; Japanese.

XX CC The invention relates to a novel variant of the hyperpolarisation

CC activated cyclic nucleotide-gated potassium channel 4 (HCN4) gene that is

CC associated with arrhythmia inducing disease. The invention further

CC comprises: a kit or composition for diagnosing the gene associated with

CC arrhythmia inducing disease, comprising the variant HCN4 gene or HCN4

CC gene; performing a method of gene therapy against arrhythmia inducing

CC disease caused by the variant HCN4 gene, involves administering the HCN4

CC gene; and an arrhythmia inducing disease animal model having a rearranged

CC variant HCN4 gene. The method is useful for performing gene therapy. The

CC variant HCN4 gene or HCN4 gene is useful for screening a pharmaceutical

CC substance against arrhythmia inducing disease. The variant HCN4 gene is

CC useful for diagnosing arrhythmia inducing disease e.g., hereditary QT

CC extension syndrome or idiopathic ventricular fibrillation. This

CC polynucleotide sequence represents a human hyperpolarisation activated

CC cyclic nucleotide-gated potassium channel 4 (HCN4) gene of the invention.

XX SQ

Query Match 69.1%; Score 927.2; DB 13; Length 5065;

Best Local Similarity 84.7%; Pred. No. 2.9e-156;

Matches 1040; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

Qy 4 TGCCTTACCAAGATCCTACGCTCTCGGCTGCTGCGCTCTCAGCTGATCCGCT 63

Db 1696 TCCGCTTACCAAGATCCTCAGCTCTTACGCTGTTAGGCTCTCGGCTCATTCGAT 1755

Qy 64 ACATCATAGTGGAGAGATCTTCCACATGACCTATGACTAGCTGGCAGCGGCTGATGA 123

Db 1756 ATATTCCACAGTGGAGAGATCTTCCACATGACCTAGACCTGGCAGCGCTGGTGC 1815

Qy 124 GGATCTGAATCTCATGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183

Db 1816 GCATCGTGAACCTCATCGCATGATGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 1875

Qy 184 TCCTGGTCCCATGCTGCGAGACTTCCCGCGCAACTGCTGGGTGTCCATCAATGCGATGG 243

Db 1876 TCCTGGTACCCATGCTACAGGACTTCCCTGAGGACTGCTGGGTGTCCATCAACATGG 1935

Qy 244 TGAACCACTCGTGGAGTGAACTGTACTCTTCCGACTCTTCAAGGCCATGAGCCATGC 303

Db 1936 TGAACCACTCTCTGGGGAAGCAGTAGTACTCTCTACGCGCTCTTCAAGGCCATGAGCCATGC 1995

Qy 304 TGTGATCGGGTACCGCGGAGGCGCCGAGAGATGACGACATCTCGCTGACCATGC 363

Db 1996 TGTGATCGGGTACCGCGGAGGCGCCGCTGGGATGTCCGAGCTCTGGCTCACCATGC 2055

Qy 364 TCAGCATGATTGTGGGTGCCACTTGTACCGCATGTTTCATCGGCGCAAGCATGCGCTCA 423

Db 2056 TCAGCATGATCTGGGTGCCACTTGTACGCCATGTTTCATCGGCGCAAGCATGCGCTCA 2115

Qy 424 TCAGTGTGTGACTCTCTCGCGCGCAGTACAGAGAGATACAGAGAGTGGAGCAGT 483

Db 2116 TCAGTGTGTGACTCTCTCGCGCGCAGTACAGAGAGTACAGAGAGTGGAGCAGT 2175

Qy 484 ACATGTCTTCCACAAGCTGCCAGCTGACTTCCGCCAGAAAGATCCACGACTACTATGAGC 543

Db 2176 ACATGTCTTCCACAAGCTGCCAGCTGACTTCCGCCAGAAAGATCCACGACTACTATGAGC 543

Qy 544 ACCGTTTACCAGGGCAAGATGTTTTCAGAGGACAGCATCTCGGCGAGAGTCTAAAGCGGCC 603

Db 2236 ACCGTTTACCAGGGCAAGATGTTTTCAGAGGAGAGCATCTCGGCGAGAGTCTAAAGCGGCC 2295

Qy 604 TCGGGAGAGATCGTCAACTTCACTGCCGAGAGCTGTGGCTTCATGCCGCTGTTCG 663

Db 2296 TCGGGAGAGATCATCAACTTTAACTGTCGGAAGCTGGTGGCTTCATGCCACTGTGTTG 2355

Qy 664 CCAACGCCAGCCCAACTTTCGTCACGGCATCTGACCAAGCTCAAGTTCGAGGTCTTCC 723

Db 2356 CCAATGCGAGCCCAACTTTCGTCGACGTCTGTCACCAAGCTGCGTTTCGAGGTCTTCC 2415

Qy 724 AGCGGCTGACTACATCATCTCCGGAAGGACCATCGGGAAGAGATGTACTTCATCCAGC 783

Db 2416 AGCGGCTGACTACATCATCTCCGGAAGGACCATTCGGAAGAGATGTACTTCATCCAGC 2475

Qy 784 AGCGGCTGTCAGCTGCTCACTAAGGGCAACAGAGAGATGAAGCTGTTCGATGGCTCT 843

Db 2476 ATGGCTGCTGTCAGCTGCTCACTAAGGGCAACAGAGAGATGAAGCTGTTCGATGGCTCT 2535

Qy 844 ACTTCGGGAGATCTGCTGCTCACTCCCGGGCGCGCAGCGAGCTGCGGCTGACA 903

Db 2536 ACTTCGGGAGATCTGCTGCTCACTCCCGGGCGCGCAGCGAGCTGCGGCTGACA 2595

Qy 904 CCTACTGCGGCTCTTATTCGCTGAGGCTGGACAACTTCAACGAGGTGCTGGAGAGTACC 963

Db 2596 CCTACTGCGGCTCTTATTCGCTGAGGCTGGACAACTTCAATGAGGTGCTGGAGAGTACC 2655

Qy 964 CCATGATGCGGCGGCTTTCGAGACGCTGGCCATTCGACCGCTGAGCCGATCGGCAAGA 1023

Db 2656 CCATGATGCGAAGGGCTTTCGAGACGCTGGCGCTGGACCGCTGGACCGCTTGGCAAGA 2715

Qy 1024 AGAATTCATCTCTTCGACAAAGTGCAGCATGACCTCAACTCGGGGCTATTCAACAAC 1083

Db 2716 AGAATTCATCTCTTCGACAAAGTGCAGCATGACCTCAACTCGGGGCTATTCAACTACC 2775

Qy 1084 AGAGAAAGCCATCATCTCAGAGATCGTCAAGTACGACCGCGAGATGGTGCAGAGCCG 1143

Db 2776 AGAGAAATGATCATCTCAGAGATGGTGCAGATGACCGGAGATGCGCCACTGCGCGC 2835

Qy 1144 AGCTGGGCTCAGCGGCTGGGCTCTTTCGCGCGCGCGCGCGCGCGCGCTGACCTCGG 1203

Db 2836 ACCGCTTCCAGGCTGCTGCTCTGCGCACCCCAACCCCAAGCCGCTCATCTGGAGCCCGC 2895

Qy 1204 CCATGCGCAAGCTGCGAGCGCGCGC 1231

Db 2896 TGATCCAGGCAACACTGCGGCTGCCG 2923

AC ABA09197;  
XX 11-JAN-2002 (first entry)  
XX Human cation channel hHCN4 homologue cDNA, S9Q ID NO:973.  
DE Human; cytokine; cell proliferation; cell differentiation; growth factor;  
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;  
KW inhibin; chemotaxis; chemokines; thrombolytic; oncogenesis;  
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;  
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
KW chronic inflammatory condition; proliferative retinopathy;  
KW atherosclerosis; coronary heart disease; arterial ischaemia;  
KW bone disorder; osteoporosis; vascular growth disorder;  
KW tissue regeneration; wound healing; infection; immune disorder;  
KW cell culture; drug screening; gene therapy; antiinflammatory;  
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;  
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;  
KW antifungal; vulnery; antiulcer; ss.  
XX Homo sapiens.  
XX WO200157188-A2.  
XX 09-AUG-2001.  
XX 05-FEB-2001; 2001WO-US003800.  
XX 03-FEB-2000; 2000US-00496914.  
XX 27-APR-2000; 2000US-00560875.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Liu C, Drmanac RT;  
XX WPI: 2001-457740/49.  
XX P-PSDB; ABB11953.  
XX Human proteins and DNA encoding sequences useful for preventing, treating  
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis  
PT and cancer.  
XX Claim 1; Page 830-832; 1963pp; English.  
XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and  
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
CC invention also relates to vectors and recombinant host cells comprising a  
CC nucleotide of the invention, methods of producing the novel polypeptides,  
CC antibodies against the polypeptides, methods of detecting the nucleotides  
CC or polypeptides in a sample, and methods of identifying compounds which  
CC bind to polypeptides of the invention. Although novel, many of the  
CC polypeptides of the invention have homology to known proteins, thereby  
CC giving an insight into their probable biological activities, and hence  
CC potential therapeutic applications. The polypeptides of the invention may  
CC have various activities, including cytokine, cell proliferation or cell  
CC differentiation activities; stem cell growth factor activity;  
CC haematopoiesis regulatory activity; tissue growth activity;  
CC immunomodulatory activity; activin- or inhibin-related activities;  
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
CC thrombolytic activities; receptor or ligand activities; or may be  
CC involved in oncogenesis, cancer cell proliferation or metastasis.  
CC depending on their biological activities, polypeptides and nucleotides of  
CC the invention are useful for preventing, treating or ameliorating medical  
CC conditions, e.g., by protein or gene therapy. Such conditions include  
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
CC vascular growth. Polypeptides involved with tissue regeneration and  
CC repair (for nucleic acids encoding them) may be used to promote wound  
CC healing (e.g., of burns, incisions and ulcers), while those with  
CC immunomodulatory activities may be used in the treatment of viral,  
CC bacterial and fungal infections in addition to immune disorders.

CC Polypeptides with growth factor activity may be used in cell cultures to  
CC promote cell growth. For example, such polypeptides may be used to  
CC manipulate stem cells in culture to give rise to neuroepithelial cells  
CC that can be used to augment or replace cells damaged by illness,  
CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
CC may also be used in the diagnosis of the above conditions, and in drug  
CC screening techniques. The present sequence represents a cDNA encoding a  
CC novel human polypeptide of the invention  
XX  
SQ Sequence 5499 BP; 1003 A; 1927 C; 1635 G; 934 T; 0 U; 0 Other;  
Query Match 69.1%; Score 927.2; DB 4; Length 5499;  
Best Local Similarity 84.7%; Pred. No. 2.9e-156;  
Matches 1040; Conservative 0; Mismatches 188; Indels 0; Gaps 0;  
QY 4 TCGCGTTTCCACCAAGATCTCTCAGCTCTTCGGGCTGCTGCGCTCTCTCAGCGCTGATCGCT 63  
DB 2128 TCCGCTTCCACGAAGATCTCTCAGCTCTTACGCTCTTACGCTCTTCCGCTCTCATTCGAT 2187  
QY 64 ACATCCATCAGTGGGAGGAGATCTTCCACATGACCTATGACCTGGCCAGCGGCTGATGA 123  
DB 2188 ATATTACACGAGTGGGAGGAGATCTTCCACATGACCTATGACCTGGCCAGCGGCTGATGA 2247  
QY 124 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCATCTGGGACGCGCTGCTGCAGT 183  
DB 2248 GCATCGTGAACCTCATCGGATGATGCTCTCTGCTCTGCGCATGGGACGCGCTGCTGCAGT 2307  
QY 184 TCCTGGTCCCATGCTGCAGGACTTCCCGCGCAACTGCTGGGTGTCATCAATGGCATGG 243  
DB 2308 TCCTGGTACCATGCTACAGGACTTCCCTGACGACTGCTGGGTGTCATCAACAACTGG 2367  
QY 244 TGAACCACTCGTGAGTGAACTGTACTCTTTCGCACTCTTCAAGGCCATGAGCCACATGC 303  
DB 2368 TGAACCACTCTTGGGGGAAAGCAGTACTCTTCAAGGCCATGAGCCACATGC 2427  
QY 304 TGTGATCGGTACGCGCGGCGGCGGCGGAGAGCATGACGAGCATCTGGGCTGACCATGC 363  
DB 2428 TGTGATCGGTACGCGCGGCGGCGGCGGAGAGCATGACGAGCATCTGGGCTGACCATGC 2487  
QY 364 TCAGCATGATGTGGGTGCCACCTGCTACGCCATGTTTATCGGCCACGCCCATCTGCCCTCA 423  
DB 2488 TCAGCATGATGTGGGTGCCACCTGCTACGCCATGTTTATCGGCCACGCCCATCTGCCCTCA 2547  
QY 424 TCCAGTCTGCTGCTCTCGGCGGCGGCGGCGGAGAGCATGACGAGCATCTGGGCTGAGCAGT 483  
DB 2548 TCCAGTCTGCTGCTCTCGGCGGCGGCGGCGGAGAGCATGACGAGCATCTGGGCTGAGCAGT 2607  
QY 484 ACATGCTCTTCCACCAAGCTGCGCAGTCTTCCCGCAGAAAGATCCACGACTACTATGAGC 543  
DB 2608 ACATGCTCTTCCACCAAGCTTCCCGCAGAAAGATCCACGACTACTATGAGC 2667  
QY 544 ACCGTTACAGGGCAAGATGTTTACGAGGACAGCATCTCTGGGCGAGCTCAACGGGCCCC 603  
DB 2668 ACCGTTACAGGGCAAGATGTTTACGAGGAGAGCATCTCTGGGCGAGCTCAACGGGCCCC 2727  
QY 604 TCGGGGAGAGATCGTCAACTTCACTCGCGGAGCTGCTGCTCTCAATGCGGCTGTTG 663  
DB 2728 TCGGGGAGAGATCATCAACTTTAACTGCGGAGCTGGTGGCTCTCCATGCCACTGTTG 2787  
QY 664 CCAACGCGCGACCCCAACTTTCGTGCGGCGCATGCTGACCAAGCTCAAGTTTCAGAGTCTTCC 723  
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DB 2848 AGCTGGGGACTTACATCATTCGCGAAGGACCATCGGGAAGAGATGATCTTTCATCCAGC 2907  
QY 784 AGCGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843  
DB 2908 ATGGCGTGGTTCAGCGTGTCTCAACAAAGGGCAACAGGAGACCAAGCTGGCGGCGGCTCTCT 2967  
QY 844 ACTTCGGGGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 903

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Db 2968 ACTTTGGAGAGATCTGCTGCTGACCCGGGGCCGGCCACAGCCAGCGTGAGGGCCGACA 3027
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Db 3028 CCTACTGCGCCCTCTACTGCTGAGCGTGGACAACTTCAATGAGGTGCTGGAGGATACC 3087
Qy 964 CCATGATGCGGCGCGCTTTCGAGACGCTGGCCATCGACCGCCTGGACCCGCGCATCGGCAAGA 1023
Db 3088 CCATGATGCGAAGGSCCTTCGAGACCGTGGCGCTGGACCCGCTGGACCGCATTTGGCAAGA 3147
Qy 1024 AGAATTCATCTCTCTGCAAGGTGAGCATGACCTCAACTCGGGCGGTATTCAACAACC 1083
Db 3148 AGAACTCCATCTCTCTCCACAAAGTCCAGCAGACCTCAACTCCGGCGTCTTCAACTACC 3207
Qy 1084 AGGAGAACGCCATCATCCAGGAGATCGTCAAGTACGACCGCGAGATGGTGACAGGCGCG 1143
Db 3208 AGGAGAAATGAGATCATCCAGCAGATTTGTGCAGCATGACCGGGAGATGGCCCACTGCGCGC 3267
Qy 1144 AGCTGGGCTCAGCGCGTGGGCTCTTCCCGCCGCGCGCGCGCGCGCGCGAGTCACCTCGG 1203
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Qy 1204 CCATCGCCACGCTGCAGCAGCGCGCGC 1231
Db 3328 TGATCCAGGCACCACTGCAGGCTGCCGC 3355
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OM nucleic - nucleic search, using sw model  
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(without alignments)  
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Sequence: 1 cgttgcttcaacgaatc.....cactgchgcnctcacc 1342

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues  
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2:	gb_est2.*	
3:	gb_hc.*	
4:	gb_est3.*	
5:	gb_est4.*	
6:	gb_est5.*	
7:	gb_est6.*	
8:	gb_gest1.*	
9:	gb_gest2.*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1222.4	91.1	1794	3	BC039619 Homo sapi
2	736.8	54.9	913	6	CA488537 AGENCOURT
3	723.2	53.9	829	4	BI490383 603031868
4	719	53.6	3226	3	BC039156 Mus muscu
5	719	53.6	3265	3	AK032225 Mus muscu
6	719	53.6	4015	3	AK082719 Mus muscu
7	688.2	51.3	1620	9	AI399924 Homo sapi
8	687.4	51.2	815	2	BE546989 Mus muscu
9	656.8	48.9	1638	9	AY399926 Mus muscu
10	646	48.1	785	4	BG974320 AGENCOURT
11	587	43.7	707	7	CK358214 AGENCOURT
12	585.2	43.6	691	2	AW073171 Mus muscu
13	541	40.3	564	6	CA842988 Mus muscu
14	532.2	39.7	569	6	CB054837 NISC gm06
15	532.2	39.7	569	6	CB054838 NISC gm06
16	531.6	39.6	560	7	CK902966 ir27f10.y
17	527	39.3	595	2	BF593827 nac05402
18	526.6	39.2	568	1	AI809833 wh77G04.x
19	526	39.2	542	7	CK902965 ir27f10.x
20	523.6	39.0	659	7	CF253024 mdv004.b0
21	483	36.0	520	2	BF510959 UI-H-B14-
22	473	35.2	957	6	BV714221 BV714221
23	471.4	35.1	1888	3	AK014722 Mus muscu
24	462.4	34.5	1120	5	BU956439 AGENCOURT

25	455.2	33.9	785	7	CNS28592	UI-M-HQ0-
26	452.6	33.7	1620	9	AY399925	Pan trogl
27	451.8	33.7	780	2	BE260963	601151693
28	446.4	33.3	484	1	AI422949	tf23a05.x
29	443.6	33.1	453	6	CA842473	ir27f10.y
30	438.6	32.7	509	1	AA843273	aj16503.8
31	434.4	32.4	673	6	CB556893	AMGNNUC.N
32	433.8	32.3	954	6	CB201579	AGENCOURT
33	429.8	32.0	702	7	CF531532	UI-M-FY0-
34	425.8	31.7	606	7	CV030457	Full
35	424.4	31.6	499	5	BE279829	BK279829
36	423.2	31.5	1087	2	BE798933	601583714
37	419.6	31.3	1263	9	AY401918	Mus muscu
38	416.8	31.1	858	2	BE793179	601581483
39	411.2	30.6	965	4	BI490063	603031868
40	411	30.6	785	5	BK972016	BK872016
41	403.4	30.1	974	5	BU914463	AGENCOURT
42	391.6	29.2	484	2	BE138253	UG50403.y
43	389.8	29.0	452	5	BK282916	BK282916
44	389.8	29.0	452	7	CR742764	CR742764
45	380.6	28.4	1266	9	AY401916	Homo sapi

ALIGNMENTS

RESULT 1	BC039619	1794 bp	mRNA	linear	HTC 19-NOV-2003
LOCUS	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 2, mRNA (cdna clone IMAGE:5730201).				
DEFINITION	BC039619				
ACCESSION	BC039619.1				
VERSION	GI:24464597				
KEYWORDS	HTC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1794)				
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagnier,L., Shenmen,C.M., Schuler,G.D., Altshuler,S.F., Zeeberg,B., Buotow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diachenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carrinci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahy,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
MEDLINE	22388257				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 1794)				
AUTHORS	Strausberg,R.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>				
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgabs-r@mail.nih.gov">cgabs-r@mail.nih.gov</a> Tissue Procurement: Invitrogen				



cdNA Library Preparation: Life Technologies, Inc.  
cdNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Institute for Systems Biology  
http://www.systemsbio.org  
Contact: amadan@systemsbiology.org  
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 84 Row: j Column: 20  
This clone has the following problem: no polyA-tail.

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ORIGIN

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Db 603 ACATCATCAGTGGGAGGAGATCTTCCACATGACCTATGACCTTGGCAGCGGCTGATGA 662  
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Db 783 TGAACCACTCGTGGAGTGAATGTACTCTTGGCACTCTTCAAGGCGCATGAGCCATGCG 842  
304 TGTGCTACGGGTACGGCGCGCAGGCGCCGAGAGCATGACGACATCTGGCTGACCATGC 363  
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Db 963 TCCAGTCTGCTGCACTCTCTCGCGCGCCAGTACAGGAGAGTACAGAGAGTGGAGCACT 1022  
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Db 1023 ACATGTCCTTCCAGAGCTGCGAGCTGACTTCCGCGCAGAGATCCACGACTACTATGAGC 1082  
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DEFINITION mRNA sequence.  
ACCESSION CA488537  
VERSION CA488537.1 GI:24950678  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 913)  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Kristi A. Egland, Ira Pastan  
cdNA Library Preparation: Invitrogen Corp  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM14279 row: j column: 15  
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Subtracted with brain, liver, lung, kidney and muscle.  
Directionally cloned. Priming method: oligo-dT. Average  
insert size: 1800 bp. Library amplification: 26,000 fold.  
Kristi A. Eglund, James J. Vincent, Robert Strausberg,  
Bungkook Lee & Ira Pastan: Discovery of new breast  
cancer genes encoding membrane and secreted proteins.  
Manuscript submitted."

ORIGIN		Query Match	54.9%;	Score 736.8;	DB 6;	Length 913;
		Best Local Similarity	96.3%;	Pred. No. 1.1e-140;		
		Mismatches 787;	Conservative 0;	Mismatches 23;	Indels 7;	Gaps 3;
QY	81	GAGATCTTCACATGACCTATGACCTGGCCAGCGCGTGGATGAGGATCTGCAATCTCATC	140			
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QY	141	AGCATGATGCTGCTCTGCCACTCGGACGGCTGCTGAGTCTCTGCTGCTGCTGCTGCTG	200			
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QY	201	CAGGACTTCGCGGCAACTGCTGGTGTTCATCAATGGCATGCTGTAACCACTCGTGAGT	260			
DB	121	CAGGACTTCGCGGCAACTGCTGGTGTTCATCAATGGCATGCTGTAACCACTCGTGAGT	180			
QY	261	GAACTGTACTCTTCGCACTCTTCAAGGCCATCAGCCACATGCTGTGCTACGGGTACGGC	320			
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QY	321	CGCAGCGCGCCGAGAGCATGACGACATCTGGCTGACCAATGCTCAGCATGATTTGGGT	380			
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QY	381	GCCACTGTGTAACGATGTTTCATCGGCGACGCACTGCTCTCATTCAGTCTGCTGCTCC	440			
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QY	441	TCGCGGCGCGGATACGAGGAGTACAGCAGTGGAGGAGTACATGCTCTTCCCAAG	500			
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QY	561	ATGTTTCAGGAGACAGCATCTTGGGCGAGTCAACCGGCGCTTGGGGAGGAGATGCTC	620			
DB	481	ATGTTTCAGGAGACAGCATCTTGGGCGAGTCAACCGGCGCTTGGGGAGGAGATGCTC	540			
QY	621	AATTTCAACTGCGGAGAGTGGTGGCTTCCATGCGCTGTTCGCAACGCGACCCCAAC	680			
DB	541	AATTTCAACTGCGGAGAGTGGTGGCTTCCATGCGCTGTTCGCAACGCGTACCCCAAC	600			
QY	681	TTGCTCACGGCATGCTGACCAAGTCAAGTTCAGGCTTTCAGCGCGGTGACTATATC	740			
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QY	741	ATCCGCGAAGGCA-CCATCGGGAAGAAGATGTAATTCATCAGCACCGCGTGTGACGCT	799			
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QY	800	GCTCACTAAGGCAACAG-AGATGAGCTGTCCGATGCTCTACTCTCGGGAGATCT	858			
DB	721	GCTCACTAAGGCAACAGAGATATAAACCCTGTCCGATGGCTCTTAATCTCGGGGAGAT	780			
QY	859	GCCTGCT-----CACCCGGGCGCCCGCAGCGGCGAGC	890			
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RESULT 3  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

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mRNA sequence.  
BI490383  
BI490383.1 GI:15329611  
EST.  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NIH-MGC <http://mgc.ncl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)  
cDNA Sequencing by: Incyte Genomics, Inc.  
DNA Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
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High quality sequence stop: 824.  
Location/Qualifiers

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pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
source anonymous pool of 6 male brains, age range 23-27; 1  
male lung, age 27; and 1 male testis, age 69. Library is  
oligo-dT primed and directionally cloned (EcoRV site is  
destroyed upon cloning). Average insert size 1.8 kb,  
insert size range 1-3 kb. Library is normalized and  
enriched for full-length clones and was constructed by C.  
Gruber (Invitrogen). Research Genetics tracking code  
021. Note: this is a NIH\_MGC Library."

FEATURES  
source

1. .829  
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/mol\_type="mRNA"  
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/clone="IMAGE:5172928"  
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/note="Organ: pooled brain, lung, testis; Vector:  
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
source anonymous pool of 6 male brains, age range 23-27; 1  
male lung, age 27; and 1 male testis, age 69. Library is  
oligo-dT primed and directionally cloned (EcoRV site is  
destroyed upon cloning). Average insert size 1.8 kb,  
insert size range 1-3 kb. Library is normalized and  
enriched for full-length clones and was constructed by C.  
Gruber (Invitrogen). Research Genetics tracking code  
021. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match		53.9%;	Score 723.2;	DB 4;	Length 829;
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QY	432	CTGACTCTCTCGCGGCGCCAG-TACCAGGAGAGTACAGCAGGTGAGCAGTACATGTC	490		
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QY	491	CTTCCACAGCTGCCAGC-TGACTTCCGCCAGAGAT-CCACGACTACTATGAGCACCGT	548		
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QY	549	TACCAGGCAAGATGTTTACAGGAGACAGCA-TCCTGGGCGAGCTCAACGGGCCCCCTGGC	607		
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ACCESSION			
BC039156			
VERSION			
BC039156.1 GI:24657642			
KEYWORDS			
HTC.			
SOURCE			
Mus musculus (house mouse)			
ORGANISM			
Mus musculus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
1 (bases 1 to 3226)			
REFERENCE			
Strausberg, R.			
Direct Submission			
Submitted (01-NOV-2002) National Institutes of Health, Mammalian			
Gene Collection (MGC), Cancer Genomics Office, National Cancer			
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,			
USA			
NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>			
Contact: MGC help desk			
Email: <a href="mailto:cgabbs-r@mail.nih.gov">cgabbs-r@mail.nih.gov</a>			
Tissue Procurement: The Cepko Laboratory			
CDNA Library Preparation: Life Technologies, Inc.			
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by: Baylor College of Medicine Human Genome			
Sequencing Center			
Center code: BCM-HGSC			
Web site: <a href="http://www.hgsc.bcm.tmc.edu/cdna/">http://www.hgsc.bcm.tmc.edu/cdna/</a>			
Contact: <a href="mailto:ang@bcm.tmc.edu">ang@bcm.tmc.edu</a>			
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louseged, H.,			
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,			
A.N., Gibbs, R.A.			
Clone distribution: MGC clone distribution information can be found			
through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>			

Series: IRAK Plate: 31 Row: n Column: 14			
This clone was selected for full length sequencing because it			
passed the following selection criteria: matched mRNA gi: 6680190			
This clone has the following problem: frame shifted.			
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Db	851	TGTTGCCCATGCTGAGGACTTCCGCGCAACTGCTGGGTGCTCATTAATGGCATGGTGA	910
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QY	607	GGGAGGAGATCGTCAACTTCAACTGCGGAGGCTGGTGGCGCTCCATGCGGCTGTTTCGCA	666
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ACCESSION	AK032225		
VERSION	AK032225.1 GI:26328056		
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ORGANISM	Mus musculus		
REFERENCE	1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalisation and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
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AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409, 685-690 (2001)		
REFERENCE	5		
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
JOURNAL	Nature 420, 563-573 (2002)		
REFERENCE	6 (bases 1 to 3265)		

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayate, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imokani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://phantom.gsc.riken.jp/.

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prepare mouse tissues.  
Please visit our web site for further details.  
URL:http://genome.gsc.riken.jp/  
URL:http://fantom.gsc.riken.jp/.

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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1620)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
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VERSION BE546989.1 GI:9775634
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JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 1638)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
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 Adams,M.D. and Cargill,M.

TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering  
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 ORGANISM Mus musculus





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 Melton,D., Brown,J., Kenty,G., Permut,A., Lee,C., Kaestner,K.,  
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 Cardenas,M., Gibbons M., McCann,R., Cole,R., Teagareishvili,R.,  
 Williams,T., Jackson,Y. and Bowers,Y.  
 Endocrine Pancreas Consortium  
 Unpublished (2000)  
 Other ESTs: ir27f10.y1  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@biohp.harvard.edu  
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
 Washington University Genome Sequencing Center For information on  
 obtaining a clone please contact: Dr. Hiroshi Inoue  
 (hinoue@im.wustl.edu)  
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 Amplified once. Contact information: Hiroshi Inoue, MD,  
 Metabolism Div. (Alan Permut Lab), Washington University  
 School of Medicine, Box 8127, 660 South Euclid Ave., St.  
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:  
 314-362-1916, Fax: 314-747-2692."

## FEATURES

source

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 ACCESSION  
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 VERSION  
 CB054837.1 GI:27793124  
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 SOURCE  
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 ORGANISM  
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 1 (bases 1 to 569)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 cDNA Library Preparation:  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC)  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 info@image.llnl.gov  
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strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGCGGCATATCTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

ORIGIN
Query Match 39.7%; Score 532.2; DB 6; Length 569;
Best Local Similarity 99.1%; Pred. No. 9.8e-99;
Matches 556; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AUTHORS 1 (bases 1 to 569)
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
CDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
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infoimage.llnl.gov
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TGTACCAATCTGAAGTGGAGCGCGGCATATCTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

ORIGIN
Query Match 39.7%; Score 532.2; DB 6; Length 569;
Best Local Similarity 99.1%; Pred. No. 9.8e-99;
Matches 556; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 691 CATTGCTGACCAAGCTCAAGTTCGAGGCTTCCAGCGCGGTGACTACATCATCCGGAAG 750
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  /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGCGGCATATCTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

ORIGIN
Query Match 39.7%; Score 532.2; DB 6; Length 569;
Best Local Similarity 99.1%; Pred. No. 9.8e-99;
Matches 556; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 691 CATTGCTGACCAAGCTCAAGTTCGAGGCTTCCAGCGCGGTGACTACATCATCCGGAAG 750
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ACCESSION CB054838
VERSION CB054838.1 GI:27793125
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Qy 1171 CGCGCGCGCGCGCGCGCGCA-GTCACCTGGGCCATGCCACACGCTGCAGCAGGCGGG 1229
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1297	96.6	3372	4	US-09-949-016-165 Sequence 165, App
3	1207	89.9	1792	4	US-09-086-436-40 Sequence 40, Appl
4	1194.4	89.0	1790	4	US-08-997-685A-11 Sequence 11, Appl
5	927.2	69.1	4276	4	US-09-949-016-4900 Sequence 4900, Ap
6	927.2	69.1	5065	4	US-09-949-016-744 Sequence 744, App
7	874.2	65.1	1512	4	US-09-086-436-32 Sequence 32, Appl
8	871	64.9	1584	4	US-08-997-685A-3 Sequence 3, Appli
9	751.8	56.0	2976	4	US-09-774-528-317 Sequence 317, App
10	735.2	54.8	2733	4	US-08-997-685A-1 Sequence 1, Appli
11	706	52.6	1518	4	US-09-086-436-34 Sequence 34, Appl
12	688.8	51.3	1507	4	US-08-997-685A-5 Sequence 5, Appli
13	680.2	50.7	2246	4	US-09-086-436-38 Sequence 38, Appl
14	680.2	50.7	2263	4	US-08-997-685A-9 Sequence 9, Appli
15	680.2	50.7	3224	4	US-09-774-528-238 Sequence 238, App
16	666.6	49.7	1307	3	US-09-172-422-3 Sequence 3, Appli
17	331.8	24.7	1083	4	US-09-270-767-1038 Sequence 1038, Ap
18	331.8	24.7	1083	4	US-09-270-767-16320 Sequence 16320, A
19	285.6	21.3	31467	4	US-09-949-016-13134 Sequence 13134, A
20	285.6	21.3	31868	4	US-09-949-016-11907 Sequence 11907, A
21	221.6	16.5	601	4	US-09-949-016-21135 Sequence 21135, A
22	221.6	16.5	601	4	US-09-949-016-47503 Sequence 47503, A
23	221.2	16.5	601	4	US-09-949-016-21136 Sequence 21136, A
24	221.2	16.5	601	4	US-09-949-016-47504 Sequence 47504, A
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ALIGNMENTS

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; Patent No. 6812339  
; GENERAL INFORMATION:  
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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
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; TYPE: DNA  
; ORGANISM: Human  
; US-09-949-016-1392

Query Match	96.8%	Score 1298.6;	DB 4;	Length 3235;
Best Local Similarity	99.1%	Pred. No. 1.9e-257;		
Matches 1329;	Conservative	7;	Mismatches 2;	Indels 3;
Gaps	3;			
QY	4	TGGCTTACCAAGATCCTCAGCCTCTCGGCTGCTGGCCTCTCAGCCTGATCGCT	63	
Db	875	TGGCTTACCAAGATCCTCAGCCTCTCGGCTGCTGGCCTCTCAGCCTGATCGCT	934	
QY	64	ACATCATCAGTGGGAGGAGATCTCCATGATACCTATGACCTGGCAGCGCGGTGATGA	123	
Db	935	ACATCATCAGTGGGAGGAGATCTCCATGATACCTATGACCTGGCAGCGCGGTGATGA	994	
QY	124	GGATCTGCAATCTCATCAGCATGATGCTGCTGTCTGCGCACTGGAGCGGCTGCGTGCAGT	183	
Db	995	GGATCTGCAATCTCATCAGCATGATGCTGCTGTCTGCGCACTGGAGCGGCTGCGTGCAGT	1054	
QY	184	TCTGTGTCCTGCTGTCAGGACTTCCGCGCACTGCTGGGTGTCCTCAATGGGATGG	243	
Db	1055	TCTGTGTCCTGCTGTCAGGACTTCCGCGCACTGCTGGGTGTCCTCAATGGGATGG	1114	
QY	244	TGAACCACTGCTGGAGTGAACCTGCTTCTTCCACTCTTCAAGGCGCATGAGCCACATGC	303	
Db	1115	TGAACCACTGCTGGAGTGAACCTGCTTCTTCCACTCTTCAAGGCGCATGAGCCACATGC	1174	
QY	304	TGTGTCATCGGCTACGGCGCGCAGCGCCGAGAGCATGACGGACATCTGCTGACCATGC	363	



|||||  
1175 TGTGCATCGGGTACGCGCGGAGCGCGCGGAGAGCATGCGCTGACATGC 1234  
|||  
364 TCAGCATGATTGGGTGCCACCTGCTACGCCATGTTTCATCGGCCACGCACTGCGCTCA 423  
|||  
1235 TCAGCATGATTGGGTGCCACCTGCTACGCCATGTTTCATCGGCCACGCACTGCGCTCA 1294  
|||  
424 TCAGTGCCTGACTCTCGCGCGCCAGTACACAGAGAAGTACAAAGCAGGTGGAGCAGT 483  
|||  
1295 TCAGTGCCTGACTCTCGCGCGCCAGTACACAGAGAAGTACAAAGCAGGTGGAGCAGT 1354  
|||  
484 ACATGTCCTTCCACAGCTGCCAGCTGACTTCGCCAGAGAATCCACGACTACTATGAGC 543  
|||  
1355 ACATGTCCTTCCACAGCTGCCAGCTGACTTCGCCAGAGAATCCACGACTACTATGAGC 1414  
|||  
544 ACCGTTTACCAGGCGAAGATGTTTGACGAGGACAGCATCTCGGCGAGCTCAACGGGCCCC 603  
|||  
1415 ACCGTTTACCAGGCGAAGATGTTTGACGAGGACAGCATCTCGGCGAGCTCAACGGGCCCC 1474  
|||  
604 TCGGGAGAGATCGTCAACTTCAACTGCGGGAAGCTGTGTGGCTTCATGCGCGTGTTCG 663  
|||  
1475 TCGGGAGAGATCGTCAACTTCAACTGCGGGAAGCTGTGTGGCTTCATGCGCGTGTTCG 1534  
|||  
664 CCAAGCCGACCCCACTTCGTCACGCGCATCTGACCAAGCTCAAGTTTCGAGGTCCTCC 723  
|||  
1535 CCAAGCCGACCCCACTTCGTCACGCGCATCTGACCAAGCTCAAGTTTCGAGGTCCTCC 1594  
|||  
724 AGCGGGTGACTACATCATCCGGAAGGACCATCGGGAAGAGATGTATTTTCATCCAGC 783  
|||  
1595 AGCGGGTGACTACATCATCCGGAAGGACCATCGGGAAGAGATGTATTTTCATCCAGC 1654  
|||  
784 AGCGGTGTGAGCTGCTCACTAAGGGCAACAGAGAGATGAAGCTGTCGATGGCTCT 843  
|||  
1655 AGCGGTGTGAGCTGCTCACTAAGGGCAACAGAGAGATGAAGCTGTCGATGGCTCT 1714  
|||  
844 ACTTCGGGAGATCTGCTCTCACC CGGGCGCGCGCACGCGAGCTGCGGGCTGACA 903  
|||  
1715 ACTTCGGGAGATCTGCTCTCACC CGGGCGCGCGCACGCGAGCTGCGGGCTGACA 1774  
|||  
904 CTTACTGCGCCCTTATTCGCTGAGCTGGACAACTTCAACAGAGTGTGGAGGATACC 963  
|||  
1775 CTTACTGCGCCCTTATTCGCTGAGCTGGACAACTTCAACAGAGTGTGGAGGATACC 1834  
|||  
964 CATGATGCGGCGCGCTTCGAGACGCTGGCCATCGACCGCTGACCGCATCGGCAAGA 1023  
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1835 CCATGATGCGGCGCGCTTCGAGACGCTGGCCATCGACCGCTGGAACGCGCATCGGCAAGA 1894  
|||  
1024 AGAATTCATCTCTCGACACAGGTGCAGCATGACCTCAACTCGGGCGTATTCACAAACC 1083  
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1895 AGAATTCATCTCTCGACAAAGGTGCAGCATGACCTCAACTCGGGCGTATTCACAAACC 1954  
|||  
1084 AGGAGAACCCCATCATCCAGGAGATCGTCAAGTACGACCGCGAGATGTCGACGAGCGCG 1143  
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1955 AGGAGAACCCCATCATCCAGGAGATCGTCAAGTACGACCGCGAGATGTCGACGAGCGCG 2014  
|||  
1144 AGCTGGGCTCAGCGCTGGGCTCTTTCCGCGCGCGCGCGCGCGCGCGCA -GTCACTCG 1202  
|||  
2015 AGCTGGG -TCAGCGCTGGGCTCTTTCCGCGCGCGCGCGCGCGCGCGCGAGGTCACTCG 2073  
|||  
1203 GCATCGCCACGCTGCAGCAGCGCGCGCGCATGAGCTTCGCGCGCA -GTGGCGGCGCG 1261  
|||  
2074 GCATCGCCACGCTGCAGCAGCGCGCGCGCATGAGCTTCGCGCGAGGTGGCGGCGCG 2133  
|||  
1262 CTCGTGGGCGCGCTGCGCTCGCGCTCGCGCTCGTGGCGGCTGCGCGGCGCGCG 1321  
|||  
2134 CTCGTGGGCGCGCTGCGCTCGCGCTCGCGCTCGCGCTGCGCGGCTGCGCGGCGCG 2193  
|||  
1322 GCACCTGCGGCGGCTGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGGCGCGCG 1342  
|||  
2194 GCACCTGCGGCGGCTGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGGCTGCGCG 2214  
|||

US-09-949-016-165  
; Sequence 165, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 165  
; LENGTH: 3372  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-165

Query Match 96.6%; Score 1297; DB 4; Length 3372;  
Best Local Similarity 99.0%; Pred. No. 4.1e-257;  
Matches 1328; Conservative 7; Mismatches 3; Indels 3; Gaps 3;  
  
QY 4 TGCCTTCCACCAAGATCTTCAGCTCTCTGCGGCTGCTGCGCTCTTCAGCGCTGATCCGCT 63  
DB 1012 TGCCTTCCACCAAGATCTTCAGCTCTCTGCGGCTGCTGCGCTCTTCAGCGCTGATCCGCT 1071  
  
QY 64 ACATCCATCAGTGGAGGAGATCTTCCACATGACCTATGACCTGCGCAGCGGGTATGA 123  
DB 1072 ACATCCATCAGTGGAGGAGATCTTCCACATGACCTATGACCTGCGCAGCGGGTATGA 1131  
  
QY 124 GGATCTGCAATCTCATCAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183  
DB 1132 GGATCTGCAATCTCATCAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1191  
  
QY 184 TCCTGCTGCCATGCTGCAGGACTTTCGCGCGCAACTGCTGGGTGCTCAATGGCATGG 243  
DB 1192 TCCTGCTGCCATGCTGCAGGACTTTCGCGCGCAACTGCTGGGTGCTCAATGGCATGG 1251  
  
QY 244 TGAACCACTCGTGGAGTGAATGTACTCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303  
DB 1252 TGAACCACTCGTGGAGTGAATGTACTCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1311  
  
QY 304 TGTGATCGGGTACGCGCGGCGCGCGGAGAGATGACGAGCATCTGGCTGACCATGC 363  
DB 1312 TGTGATCGGGTACGCGCGGCGCGGAGAGATGACGAGCATCTGGCTGACCATGC 1371  
  
QY 364 TCAGCATGATTGTGGGTGCCACCTGCTACGCCATGTTTCATCGGCCACGCACTGCGCTCA 423  
DB 1372 TCAGCATGATTGTGGGTGCCACCTGCTACGCCATGTTTCATCGGCCACGCACTGCGCTCA 1431  
  
QY 424 TCCAGTCTGCTGAGTCTTCGCGCGCGCGCAGTACCGAGGAAGTACAAAGAGGTGGAGCAGT 483  
DB 1432 TCCAGTCTGCTGAGTCTTCGCGCGCGCGCAGTACCGAGGAAGTACAAAGAGGTGGAGCAGT 1491  
  
QY 484 ACATGTCCTTCCACAGCTGCCAGCT 543  
DB 1492 ACATGTCCTTCCACAGCTGCCAGCT 1551  
  
QY 544 ACCGTTTACCAGGCGAAGATGTTTGACGAGGACAGCATCTCGGCGAGCTCAACGGGCCCC 603  
DB 1552 ACCGTTTACCAGGCGAAGATGTTTGACGAGGACAGCATCTCGGCGAGCTCAACGGGCCCC 1611  
  
QY 604 TCGGGAGAGATCGTCAACTTCAACTGCGGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663  
DB 1612 TCGGGAGAGATCGTCAACTTCAACTGCGGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1671  
  
QY 664 CCAACGCGCGACCCCAACTTTCGTCAGGCGCATGCTGACCAAGCTCAAGTTTCGAGGTCCTTCC 723

1672 CCAACCGGACCCCACTTGGTACCGCCATGCTGACCAAGCTCAAGTTTCGAGGCTTCC 1731  
724 AGCCGGGTGATACATATCCCGGAAAGGACCAATCCGGGAAGAGATGTAATTCATCCAGC 783  
1732 AGCCGGGTGATACATATCCCGGAAAGGACCAATCCGGGAAGAGATGTAATTCATCCAGC 1791  
784 AGCCGGGTGATACATATCCCGGAAAGGACCAATCCGGGAAGAGATGTAATTCATCCAGC 843  
1792 AGCCGGGTGATACATATCCCGGAAAGGACCAATCCGGGAAGAGATGTAATTCATCCAGC 1851  
844 ACTTCCGGGAGATCTGCTGCTCAACCGGGGGCGCGCACGGGAGCGTGCAGGCTGACA 903  
1852 ACTTCCGGGAGATCTGCTGCTCAACCGGGGGCGCGCACGGGAGCGTGCAGGAGTACC 1911  
904 CTTACTCGCCGCTCTATTCGCTGAGCGTGGAGCAAACTTCAACGAGGCTGCGAGGAGTACC 963  
1912 CTTACTCGCCGCTCTATTCGCTGAGCGTGGAGCAAACTTCAACGAGGCTGCGAGGAGTACC 1971  
964 CCATGATGGGGCGGCGCTTCGAGACGGTGGCCATCGACCGCTGGACCGCATCGGCAAGA 1023  
1972 CCATGATGGGGCGGCGCTTCGAGACGGTGGCCATCGACCGCTGGACCGCATCGGCAAGA 2031  
1024 AGAATTCATCTCTCTGCAACAGGTCGAGCATGACCTCAACTCGGGCGTATTCAACAACC 1083  
2032 AGAATTCATCTCTCTGCAACAGGTCGAGCATGACCTCAACTCGGGCGTATTCAACAACC 2091  
1084 AGGAGAACCCATCATCCAGGAGATCGTCAAGTACGACCGCGAGATGGTGCAGAGCGCG 1143  
2092 AGGAGAACCCATCATCCAGGAGATCGTCAAGTACGACCGCGAGATGGTGCAGAGCGCG 2151  
1144 AGTGGGCTCAGCGCTGGGCTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1202  
2152 AGTGGG-TCAGCGCGTGGGCTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2210  
1203 GCCATGCCACGCTGCAGAGCGGGCGGCATGAGCTTTCGCCGCA-GTCACTCG 1261  
2211 GCCATGCCACGCTGCAGAGCGGGCGGCATGAGCTTTCGCCGCAAGTCACTCG 2270  
1262 CTCGTGGGCGGCTGGCGCTCGCGCTCGCGCGCTCGTGGCGHGVNDYHCCCGGGGSC 1321  
2271 CTCGTGGGCGGCTGGCGCTCGCGCTCGCGCGCTCGTGGCGCGCGCGCGCGCGCGCGCG 2330  
1322 GCACCTGCHGCGNCTCACCC 1342  
2331 GCACCTGCHGCGNCTCACCC 2351

RESULT 3

US-09-086-436-40  
; Sequence 40, Application US/09086436  
; Patent No. 6703485  
; GENERAL INFORMATION:  
; APPLICANT: Kandel, Eric R.  
; APPLICANT: Santoro, Bina  
; APPLICANT: Bartesch, Dusan  
; APPLICANT: Siegelbaum, Steven  
; APPLICANT: Tibbs, Gareth  
; APPLICANT: Grant, Seth  
; TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and  
; TITLE OF INVENTION: Uses Thereof  
; FILE REFERENCE: 0575/54806-A  
; CURRENT APPLICATION NUMBER: US/09/086,436  
; CURRENT FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 1792  
; TYPE: DNA  
; ORGANISM: Human  
US-09-086-436-40

Query Match 89.9%; Score 1207; DB 4; Length 1792;

Best Local Similarity 99.0%; Pred. No. 1.le-238;  
Matches 1235; Conservative 0; Mismatches 11; Indels 2; Gaps 2;  
QY 4 TCGCGCTTCCACCAAGATCTCTCAGCGCTTCTCGCGCTCTCGCGCTCTCTCAAGCTGATCCGCT 63  
DB 541 TCGCGCTTCCACCAAGATCTCTCAGCGCTTCTCGCGCTCTCGCGCTCTCTCAAGCTGATCCGCT 600  
QY 64 ACATCCATCAGTGGGAGGAGATCTTCCACATGACCTATGACCTGCGCAGCGCGGTGATGA 123  
DB 601 ACATCCATCAGTGGGAGGAGATCTTCCACATGACCTATGACCTGCGCAGCGCGGTGATGA 660  
QY 124 GATCTGCAATCTATCAGCATGATGCTGCTGCTCTGCGCAGCGCTGCGCTGCGCTGCGCT 183  
DB 661 GATCTGCAATCTATCAGCATGATGCTGCTGCTCTGCGCAGCGCTGCGCTGCGCTGCGCT 720  
QY 184 TCCTCGTGGCCCATCTGCGAGGACTTCCCGCGCAACTGCTGGGTGCTTCCATCAATGGCATGG 243  
DB 721 TCCTCGTGGCTATGCTGCGAGGACTTCCCGCGCAACTGCTGGGTGCTTCCATCAATGGCATGG 780  
QY 244 TGAACCACTCGTGGAGTGAATGTACTCTTCGCACTCTTCAAGGCGCATGAGCCACATGC 303  
DB 781 TGAACCACTCGTGGAGTGAATGTACTCTTCGCACTCTTCAAGGCGCATGAGCCACATGC 840  
QY 304 TGTGATCGGGTACCGCGCGGAGGCGCGCGAGAGCATGACGACATCTGGCTGACCATGC 363  
DB 841 TGTGATCGGGTACCGCGCGGAGGCGCGCGGCGCGGAGGAGTGAAGGAGTGAAGGAGTGAAG 900  
QY 364 TCAGCATGATTCGCGTGGGTCGCACTGCTAGCGCACTGTTTCATCGCGCAGCGCATCTGCGCTCA 423  
DB 901 TCAGCATGATTCGCGTGGGTCGCACTGCTAGCGCACTGTTTCATCGCGCAGCGCATCTGCGCTCA 960  
QY 424 TCCAGTCTGCGTGGAGTCTCTCGCGCGCGCAGTACAGGAGAAAGTACAAGAGAGTGGAGAGT 483  
DB 961 TCCAGTCTGCGTGGAGTCTCTCGCGCGCGCAGTACAGGAGAAAGTACAAGAGAGTGGAGAGT 1020  
QY 484 ACATGCTCTTCCACAAAGTGGCGAGTCTTCGCGCAGAGATCTCAAGAGTACTATGAGC 543  
DB 1021 ACATGCTCTTCCACAAAGTGGCGAGTCTTCGCGCAGAGATCTCAAGAGTACTATGAGC 1080  
QY 544 ACCTGTTACAGGCGCAAGATGTTTGAAGGAGAGCATCTCGCGCGAGCTCAAGCGGCGCCC 603  
DB 1081 ACCTGTTACAGGCGCAAGATGTTTGAAGGAGAGCATCTCGCGCGAGCTCAAGCGGCGCCC 1140  
QY 604 TCGCGGAGGAGATCGTCAACTTCACTGCGGAGCTGGTGGCTCCATCGCGCTGTTTCG 663  
DB 1141 TCGCGGAGGAGATCGTCAACTTCACTGCGGAGCTGGTGGCTCCATCGCGCTGTTTCG 1200  
QY 664 CCAACCGCGACCCCAACTTTCGTCACCGGCCATGCTGACCAAGCTCAAGTTCGAGGCTTTC 723  
DB 1201 CCAACCGCGACCCCAACTTTCGTCACCGGCCATGCTGACCAAGCTCAAGTTCGAGGCTTTC 1260  
QY 724 AGCGGGTGAATACATCATCCCGGAGGAGCATCCCGGAGAGAGATGTAATTCATCCAGC 783  
DB 1261 AGCGGGTGAATACATCATCCCGGAGGAGCATCCCGGAGAGAGATGTAATTCATCCAGC 1320  
QY 784 ACAGCGTGGTCAAGCGTGGCTCACTAAGGCGCAACAGGAGATGAAGCTGTCCGATGGCTCT 843  
DB 1321 ACAGCGTGGTCAAGCGTGGCTCACTAAGGCGCAACAGGAGATGAAGCTGTCCGATGGCTCT 1380  
QY 844 ACTTCGGGAGATCTGCTGCTCAACCGGGGCGCGCGCAGCGGAGGCTGCGGGCTGACA 903  
DB 1381 ACTTCGGGAGATCTGCTGCTCAACCGGGGCGCGCGCAGCGGAGGCTGCGGGCTGACA 1440  
QY 904 CTTACTCGCGCTCTTATTCGCGAGGCTGGAGCAACTTCAACGAGGCTGCTGGAGGAGTACC 963  
DB 1441 CTTACTCGCGCTCTTATTCGCGAGGCTGGAGCAACTTCAACGAGGCTGCTGGAGGAGTACC 1500  
QY 964 CCATGATGGCGCGCTTCGAGACGGTGGCCATCGACCGCTGAGCCGCGCATCGGCAAGA 1023  
DB 1501 CCATGATGGCGCGCTTCGAGACGGTGGCCATCGACCGCTGAGCCGCGCATCGGCAAGA 1560  
QY 1024 AGAATTCATCTCTCTGCAACAGGTCGAGCATGACCTCAACTCGGGGCTATTCAACAACC 1083

Db 1561 AGAATTCATCTCTCTGACAAAGGTGACGATGACCTCAACTCGGGCGTATTCAACAACC 1620  
 QY 1084 AGAGAAACCCATCATATCCAGAGATCGTCAAGTACGACCGCGAGATGTTGACAGAGCGG 1143  
 Db 1621 AGAGAAACCCATCATATCCAGAGATCGTCAAGTACGACCGCGAGATGTTGACAGAGCGG 1680  
 QY 1144 AGCTGGGCTCAGCGGTGAGGCTCTTCCCGCGCGCGCGCGCGCGCA-GTCAACCTCG 1202  
 Db 1681 AGCTGGG-TCAGCGCGTGGGCTTTTCCCGCGCGCGCGCGCGCGCGCGCGAGTCACTTCG 1739  
 QY 1203 GCATCGCCACGCTGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 1250  
 Db 1740 GCATCGCCACGCTGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 1787

RESULT 4

US-08-997-685A-11  
 ; Sequence 11, Application US/08997685A  
 ; Patent No. 6551821  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Trustees of Columbia University  
 ; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof  
 ; FILE REFERENCE: 0575/54806  
 ; CURRENT APPLICATION NUMBER: US/08/997,685A  
 ; CURRENT FILING DATE: 1997-12-12  
 ; NUMBER OF SEQ ID NOS: 60  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 11  
 ; LENGTH: 1790  
 ; TYPE: DNA  
 ; ORGANISM: human;  
 US-08-997-685A-11

Query Match 89.0%; Score 1194.4; DB 4; Length 1790;  
 Best Local Similarity 98.9%; Pred. No. 4.2e-236;  
 Matches 1234; Conservative 0; Mismatches 11; Indels 3; Gaps 3;

QY 4 TCGGCTTCAACCAAGATCTCAGCTCTCGGCTGCTGGCTCTCAAGCTGATCGGCT 63  
 Db 540 TCGGCTTCAACCAAGATCTCAGCTCTCGGCTGCTGGCTCTCAAGCTGATCGGCT 599  
 QY 64 ACATCCATCAGTGGGAGGATCTTCCACATGACCTATGACCTGCGCGGCGGATGA 123  
 Db 600 ACATCCATCAGTGGGAGGATCTTCCACATGACCTATGACCTGCGCGGCGGATGA 659  
 QY 124 GGATCTGCAATCTCATCAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183  
 Db 660 GGATCTGCAATCTCATCAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 719  
 QY 184 TCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243  
 Db 720 TCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 779  
 QY 244 TGAACCACTCGTGGAGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303  
 Db 780 TGAACCACTCGTGGAGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 839  
 QY 304 TGTGATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 363  
 Db 840 TGTGATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899  
 QY 364 TCAGCATGATGTTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423  
 Db 900 TCAGCATGATGTTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 959  
 QY 424 TCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483  
 Db 960 TCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1019  
 QY 484 ACATGCTCTTCCACAAAGCTGCCAGTGAATTCGCGCAGAAAGATCCACGACTACTATGAC 543  
 Db 1020 ACATGCTCTTCCACAAAGCTGCCAGTGAATTCGCGCAGAAAGATCCACGACTACTATGAC 1079

QY 544 ACCGTTACCGGCGAAGATGTTTGAAGAGACAGCATCTCTGGGCGAGCTCAAGCGGCCCC 603  
 Db 1080 ACCGTTACCGGCGAAGATGTTTGAAGAGACAGCATCTCTGGGCGAGCTCAACCGGCCCC 1139  
 QY 604 TCGGGGAGAGATCGTCAACTTCAACTGCCGGAAGCTGTTGGCTTCCATTCGCGCTGTTTCG 663  
 Db 1140 TCGGGGAGAGATCGTCAACTTCAACTGCCGGAAGCTGTTGGCTTCCATTCGCGCTGTTTCG 1199  
 QY 664 CCAACGCGACCCCAACTTTCGTCACGCGCATGCTGCAACAGTCAAGTTCAGAGTCTTCC 723  
 Db 1200 CCAACGCGACCCCAACTTTCGTCACGCGCATGCTGCAACAGTCAAGTTCAGAGTCTTCC 1259  
 QY 724 AGCGGGTGACTACATCATCTCCGGAAGCAGCATCGGGAAGAGTACTTTCATCCAGC 783  
 Db 1260 AGCGGGTGACTACATCATCTCCGGAAGCAGCATCGGGAAGAGTACTTTCATCCAGC 1319  
 QY 784 ACGGCTGCTCAGCGTGTCTCACTAAGGGAACAAGAGATGAAGTGTCCGATGCTCTCT 843  
 Db 1320 ACGGCTGCTCAGCGTGTCTCACTAAGGGAACAAGAGATGAAGTGTCCGATGCTCTCT 1379  
 QY 844 ACTTCGGGAGATCTGCTGCTCACTCCCGGGCGCGCGCACGCGAGCTGCGGGCTGACA 903  
 Db 1380 ACTTCGGGAGATCTGCTGCTCACTCCCGGGCGCGCGCACGCGCA-CGTGGGGCTGACA 1438  
 QY 904 CTTACTGCGGCTCTATTTCGCTGAGCTGAGCAACTTCAACAGAGTGTCTGGAGAGTACC 963  
 Db 1439 CTTACTGCGGCTCTATTTCGCTGAGCTGAGCAACTTCAACAGAGTGTCTGGAGAGTACC 1498  
 QY 964 CCATGATCGCGCGGCTTTCGAGACGCTGGGCGCATCGACGCTGCGACCGCATCGGCAAGA 1023  
 Db 1499 CCATGATCGCGGCGCTTTCGAGACGCTGGGCGCATCGACGCTGCGACCGCATCGGCAAGA 1558  
 QY 1024 AGAATTCATCTCTCTGCAAGGTGACGATGACCTCAACTCGGGCTGATTTCAACAACC 1083  
 Db 1559 AGAATTCATCTCTCTGCAAGGTGACGATGACCTCAACTCGGGCTGATTTCAACAACC 1618  
 QY 1084 AGGAGAACCCATCATCTCAGGAGATCTGCAAGTACGACCGGAGATGCTGAGCAGGCGG 1143  
 Db 1619 AGGAGAACCCATCATCTCAGGAGATCTGCAAGTACGACCGGAGATGCTGAGCAGGCGG 1678  
 QY 1144 AGCTGGGCTCAGCGGCTGCTCTTCCGCGCGCGCGCGCGCGCGCA-GTCACTCG 1202  
 Db 1679 AGCTGGG-TCAGCGGCTGGGCTTTTCCGCGCGCGCGCGCGCGCGCGCGAGTCACTTCG 1737  
 QY 1203 GCCATGCGCACGCTGACGACGCGCGCGCGCGCGCGCGCGCGAGTTCGCGCGCAG 1250  
 Db 1738 GCCATGCGCACGCTGACGACGCGCGCGCGCGCGCGCGCGAGTTCGCGCGCAG 1785

RESULT 5

US-09-949-016-4900  
 ; Sequence 4900, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4900  
 ; LENGTH: 4276  
 ; TYPE: DNA  
 ; ORGANISM: Human

US-09-949-016-4900

Query Match 69.1%; Score 927.2; DB 4; Length 4276;  
Best Local Similarity 84.7%; Pred. No. 3.6e-181;  
Matches 1040; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 4 TGGCTTTACCAAGATCCTCAGCCTCTGCGGCTGCTGGCCCTCTCAGCCCTGATCCGCT 63  
DB 849 TCGCTTTCAGGAATCCTCAGCCTCTTACGCTCTTACGCTCTTCCGCTCTCCGCTCATTCGAT 908

QY 64 ACATCCATCAGTGGGAGGATCTTCCATGACCTATGACCTGCGAGCGCGGTGATGA 123  
DB 909 ATATTACCAAGTGGGAAGATCTTCCATGACCTTACGACCTGGCAGCGCGGTGTC 968

QY 124 GATCTGCAATCTCATCAGATGATGCTGCTGCTTCCCACTGGGAGGCTGCTGCAGT 183  
DB 969 GCATCGTGAACCTCATCGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1028

QY 184 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 243  
DB 1029 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1088

QY 244 TGAACCACTCGTGGAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 303  
DB 1089 TGAACCACTCGTGGGAGCAGTACTCTTACGCTCTTCAAGGCTGCTGCTGCTGCTG 1148

QY 304 TGTGATCGGATGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 363  
DB 1149 TGTGATCGGATGAGCG 1208

QY 364 TCAGCATGATGCTGGGCGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423  
DB 1209 TCAGCATGATGCTGGGCGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1268

QY 424 TCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483  
DB 1269 TCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1328

QY 484 ACATGCTCTTCCAAAGCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543  
DB 1329 ACATGCTCTTCCAAAGCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1388

QY 544 ACCGTTACAGGCGCAAGATGTTGACGAGGAGCAGCATCTTGGGCGAGCTCAACGGG 603  
DB 1389 ACCGTTACAGGCGCAAGATGTTGACGAGGAGCAGCATCTTGGGCGAGCTCAACGG 1448

QY 604 TGGCGGAGGATCGTCAACTTCAACTTCAACTTCAACTTCAACTTCAACTTCAACTT 663  
DB 1449 TGGCGGAGGATCATCAACTTCAACTTCAACTTCAACTTCAACTTCAACTTCAACT 1508

QY 664 CCAACGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723  
DB 1509 CCAATCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1568

QY 724 AGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 783  
DB 1569 AGCGTGGGAGTATCATCATCGGAGGAGCACCATTGGCAAGAGATGATCTTATCC 1628

QY 784 AGCGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843  
DB 1629 ATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1688

QY 844 ACTTGGGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 903  
DB 1689 ACTTGGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1748

QY 904 CTTACTGCGGCTCTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 963  
DB 1749 CTTACTGCGGCTCTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1808

QY 964 CCATGATCGGCGGCTTTCAGAGCGGTGGCGCATCGACCGGCTGAGCCGCTGGAAGA 1023  
DB 1809 CCATGATCGAAGGCGCTTCAGAGCGGTGGCGCATCGACCGGCTGGAAGA 1868

RESULT 6

US-09-949-016-744  
; Sequence 744, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 744  
; LENGTH: 5065  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-744

Query Match 69.1%; Score 927.2; DB 4; Length 5065;  
Best Local Similarity 84.7%; Pred. No. 3.8e-181;  
Matches 1040; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 4 TGGCTTTACCAAGATCCTCAGCCTCTGCGGCTGCTGGCCCTCTCAGCCCTGATCCGCT 63  
DB 1696 TCGGCTTTCAGGAATCCTCAGCCTCTTACGCTGCTTACGCTCTTCCGCTCATTCGAT 1755

QY 64 ACATCCATCAGTGGGAGGATCTTCCATGACCTATGACCTGGCGAGCGCGGTGATGA 123  
DB 1756 ATATTACCAAGTGGGAAGATCTTCCATGACCTTACGACCTGCGCGGCTGCTGCTG 1815

QY 124 GATCTGCAATCTCATCAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 183  
DB 1816 GCATCTGAACCTCATCGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1875

QY 184 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 243  
DB 1876 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1935

QY 244 TGAACCACTCGTGGAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 303  
DB 1936 TGAACCACTCGTGGGAGGAGTACTCTTACGCGCTCTTCAAGGCTTCAAGGCTTCA 1995

QY 304 TGTGATCGGCTACG 363  
DB 1996 TGTGATCGGCTACG 2055

QY 364 TCAGCATGATGCTGGGTGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423

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Db      2056 TCAGCATGATCGTGGTGCACCTGCTAGCCCATGTTCAATTTGGCCAGCCACTGCGCTCA 2115
QY      424 TCAGTTCGTGACTCCTCGCGCGCCAGTACAGGAGAAAGTACAAAGAGGTGAGAGT 483
Db      2116 TCAGTTCGTGACTCCTCGCGCGCCAGTACAGGAGAAAGTACAAAGAGGTGAGAGT 2175
QY      484 ACATGTCCTTCCACAGCTGCCAGCTGACTTCGGCCGAGAGATCCAGACTACTATGAGC 543
Db      2176 ACATGTCCTTCCACAGCTGCCCGCCGACACCGCGCAGCGCATCCACGACTACTACGAGC 2235
QY      544 ACCGTTACAGGCAAGATGTTTACGAGGACAGCATCTCGCGCGAGCTCAACGCGGCCCC 603
Db      2236 ACCGTTACAGGCAAGATGTTTACGAGGAGAGCATCTCGCGCGAGCTTAAGGAGGCC 2295
QY      604 TGGGGAGAGATCGTCAACTTAACTGCGGAGAGCTGTGGCTTCCATGCCGCTGTTG 663
Db      2296 TGGGGAGAGATCATCAACTTTAACTGTGCGAAGCTGTGGCTTCCATGCCACTGTTT 2355
QY      664 CCNACGCGGACCCCACTTCGTACGCGCCATGCTGACCAAGCTCAAGTTTCGAGGTTTCC 723
Db      2356 CCNACGCGGACCCCACTTCGTGACGTCCATGCTGACCAAGCTGCGTTTCGAGGTTTCC 2415
QY      724 AGCGGGTGACTACATCATCTCCGGAAGGACCATCGGGAAGAGATGTAATTCATCCAGC 783
Db      2416 AGCGTGGGACTACATCATCTCCGGAAGGACCATTCGGAAGAGATGTAATTCATCCAGC 2475
QY      784 AGCGGTGTGTCAGCGTGCTCACTAAGGGCAACAGGAGATGAAGTGTCCGATGGTCTCT 843
Db      2476 ATGGCGTGTGTCAGCGTGCTCACTAAGGGCAACAGGAGATGAAGTGTCCGATGGTCTCT 2535
QY      844 ACTTTCGGGAGATCTGCTGCTCACCAGGCGCGCGGACGCGGAGCGTGGCGGCTGACA 903
Db      2536 ACTTTCGGGAGATCTGCTGCTCACCAGGCGCGCGGACGCGGAGCGTGGCGGCGGACA 2595
QY      904 CTTACTGCGCGCTTATTCGCTGAGGTGAGCAACTTCAACGAGGTGCTGGAGGAGTACC 963
Db      2596 CTTACTGCGCGCTTATTCGCTGAGGTGAGCAACTTCAACGAGGTGCTGGAGGAGTACC 2655
QY      964 CCATGATGCGGCGCGCTTCGAGACGGTGGCCCATCGACCGCTGGACCGCATCGGCAAGA 1023
Db      2656 CCATGATGCGGAGGCGCTTCGAGACGGTGGCCCATCGACCGCTGGACCGCATTCGCAAGA 2715
QY      1024 AGAATTCATCTCTTCGACAGGTGACGATGACCTCACTCGGCGGTATTCACCAACC 1083
Db      2716 AGAATTCATCTCTTCGACAGGTGACGATGACCTCACTCGGCGGTATTCACCAACC 2775
QY      1084 AGGAGAACGCCATCATCTCCAGGAGATCGTCAAGTACGACCGGAGATGGTGACGAGCGG 1143
Db      2776 AGGAGAATGAGATCATCTCAGCATGTTGTGAGCATGACCCGGGAGATGGCCCATCGGCGC 2835
QY      1144 AGTGGGCTCAGCGGTGGGCTCTTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1203
Db      2836 ACCGCGTCCAGGCTGCTGCTCTGCGCACCCCAACCCCAACCCCAACCCCAACCCCAAC 2895
QY      1204 CCATCCCGACGCTGACGAGGCGGCGCGC 1231
Db      2896 TGATCCAGGCACCACTGCAGGCTGCGCGC 2923

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RESULT 7

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US-09-086-436-32
; Sequence 32, Application US/09086436
; Patent No. 6703485
; GENERAL INFORMATION:
; APPLICANT: Kandel, Eric R.
; APPLICANT: Santoro, Bina
; APPLICANT: Bartsch, Dusan
; APPLICANT: Siegelbaum, Steven
; APPLICANT: Tibbs, Gareth
; APPLICANT: Grant, Seth
; TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 0575/54806-A

```

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; CURRENT APPLICATION NUMBER: US/09/086,436
; CURRENT FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Murine
; US-09-086-436-32

Query Match      65.1%; Score 874.2; DB 4; Length 1512;
Best Local Similarity 88.9%; Pred. No. 2.2e-170;
Matches 945; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY      4 TGGCGTTCCAAAGATCTCTCAGCTCTCGGGCTGCTGCGGCTCTCTCAGCGCTGATCCGCT 63
Db      449 TGGCGTTCCAAAGATCTCTCAGCTCTCGGGCTGCTGCGGCTCTCTCAGCGCTGATCCGCT 508
QY      64 ACATCCATCAGTGGGAGGAGATCTTCCACATGACCTATGACCTGCGGAGCGGAGTATGA 123
Db      509 ATATCCACAGTGGGAGGAGATTTTCCACATGACCTATGACCTGCGGAGCGGAGTATGA 568
QY      124 GGATCTGCAATCTCATCAGCATGATGCTGCTGCTCTGCGCACTGGGACCGGCTGCTGCA 183
Db      569 GCATCTGTAACTGATCAGCATGATGCTGCTCTGCGCACTGGGACCGGCTGCTGCA 628
QY      184 TCCTGGTCCCATGCTGACGAGCTTCCCGCGCAACTGCTGGGTGTCATCAATGGGATGG 243
Db      629 TCCTGGTCCCATGCTGCAAGACTTCCCGCAGCGACTGCTGGGTGTCATCAACAACTGG 688
QY      244 TGAACCACTCGTGGAGTGAATGTAATCTTCTGCGACTCTTCAAGGCCATGAGCCACATGC 303
Db      689 TGAACCACTCGTGGAGCGAGCTCTACTGTTGCGGCTCTTCAAGGCCATGAGCCACATGC 748
QY      304 TGTGATCGGGTACCGCGCGGAGCGCGCGGAGAGCATGACGAGCATCTGGCTGACCATGC 363
Db      749 TGTGATCGGGTACCGCGCGGAGCGCGCGGAGAGCATGACGAGCATCTGGCTGACCATGC 808
QY      364 TCAGCATGATTTGGGTGCGACCTGCTAGCGCATGTTTATGCGGCCACGCGCACTGCGCTCA 423
Db      809 TCAGCATGATCGTAGGCGCCACTGCTATGCCATGTTTCAATTTGGGCAACGCACTGGGCTCA 868
QY      424 TCCAGTCTCGACTCTCTCGCGCGCGGAGTACCGAGAGAGTACAAAGCAGGTGGAGCAGT 483
Db      869 TCCAGTCTCGACTCTCTCGCGCGCGGAGTACCGAGAGAGTACAAAGCAGGTGGAGCAGT 928
QY      484 ACATGTCCTTCCACAAAGTCTGCGAGTCTGCTCCGCGCAGAAATCCACGACTACTATGAGC 543
Db      929 ACATGTCCTTCCACAAAGTCTGCGCGCTGACTTCCGCGCAGAGATCCACGATTTACTAT 988
QY      544 ACCGTTACAGGCGCAAGATGTTTGAAGGAGCAGCATCTGCGGCGAGCTCAACGCGGCC 603
Db      989 ACCGTTACAGGCGCAAGATGTTTGAAGGAGCAGCATCTGCGGCGAGTCAACGCGGCCAC 1048
QY      604 TGGCGGAGGAGATCGTCAACTTCACTCGCGGAGCTGCTGCGCTCTCTCAGCGCTGTTG 663
Db      1049 TGGCGGAGGAGATCGTCAACTTCACTCGCGGAGCTGCTGCGCTCTCTCAGCGCTGTTG 1108
QY      664 CCAAGCGCGACCCCAACTTTCGTCAGCGCATGCTGACCAAGCTCAAGTTTCGAGGCTTCC 723
Db      1109 CCNATGCGAGACCCCAATTTGTCAGCCATGCTGACAAAGCTCAAAATTTGAGGCTTCC 1168
QY      724 AGCGGGTGACTTACATCATTCGCGAAGGCAACATCGGGAAGAGATGTAATTCATCCAGC 783
Db      1169 AGCGCTGGAGATTACATCATTCGAGAGGGGACCATCGGGAAGAGATGTAATTCATCCAGC 1228
QY      784 ACGGCGTGTGCTGCTGCTCACTAAGGCGCAACAGGAGATGAAGTGTCCGATGCTCTCT 843
Db      1229 ATGGGGTGTGAGCGTGTCTCAACAAAGGGCAACAGGAGATGAAGTGTCCGATGCTCT 1288
QY      844 ACTTTCGGGAGATCTGCTGCTCAGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 903
Db      1289 ATTTTCGGGAGATCTGCTTGTCTACAGAGGGGCGCGGCTACGCGCGAGCGTGGAGCTGACA 1348

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QY 904 CCTACTGCGGCTTATTGCTGAGCGTGACCAACTTCAACGAGGTGCTGGAGGATACC 963  
Db 1349 CCTACTGCGGCTTATTGCTGAGCGTGACCAACTTCAACGAGGTGCTGGAGGATACC 1408  
QY 964 CCATGATGCGGCGGCTTCCAGACGCGTGCGCCATCGACCGCTGGACCGCATCGGCAAGA 1023  
Db 1409 CCATGATGCGGCGGCTTCCAGACGCGTGCGCCATCGACCGCTGGACCGCATCGGCAAGA 1468  
QY 1024 AGAATTCATCTCTCTGACACAGGTGAGCATGACCTCAATC 1066  
Db 1469 AGAATTCATCTCTCTGACACAGGTGAGCATGACCTCAATC 1511

RESULT 8  
US-08-997-685A-3  
; Sequence 3, Application US/08997685A  
; Patent No. 6551821  
; GENERAL INFORMATION:  
; APPLICANT: The Trustees of Columbia University  
; APPLICANT: Kandel, Eric  
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof  
; FILE REFERENCE: 0575/54806  
; CURRENT APPLICATION NUMBER: US/08/997,685A  
; CURRENT FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1584  
; TYPE: DNA  
; ORGANISM: mouse;  
US-08-997-685A-3

Query Match 64.9%; Score 871; DB 4; Length 1584;  
Best Local Similarity 88.7%; Pred. No. 1e-169;  
Matches 943; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 4 TGGCGTTCACCAAGATCTCAGCTCTCGGCTGCTGGGCTCTCAGCGCTGATCGCT 63  
Db 449 TGGCGTTCACCAAGATCTCAGCTCTCGGCTGCTGGGCTCTCAGCGCTGATCGCT 508  
QY 64 ACATCCATCAGTGGGAGAGATCTTCCACATGACTATGACTGGCGGCGGCGGTGATGA 123  
Db 509 ATATCCACCATGGGAGAGATTTTCCACATGACTATGACTGGCGGCGGCGGTGATGC 568  
QY 124 GGATCTGCAATCTCATCAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 183  
Db 569 GCATCTGTAACCTGATCAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 628  
QY 184 TCCTGGTCCCATGCTGAGGACTTCCGCGCAACTGCTGGGTGCTCCATCAATGGCATGG 243  
Db 629 TCCTGGTCCCATGCTGCAAGACTTCCGCGCAACTGCTGGGTGCTCCATCAACCAATGG 688  
QY 244 TGAACCACTCGTGGAGTGAATCTGCTTCCGCACTCTTCAAGGCGCATGAGCCACATGC 303  
Db 689 TGAACCACTCGTGGAGGAGTCTTACTGCTTGGGCTCTTCAAGGCGCATGAGCCACATGC 748  
QY 304 TGTGATCGGCTACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 363  
Db 749 TGTGATCGGCTACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 808  
QY 364 TCAGCATGATGTTGGGTGCGACCTGCTAGCGCATGTTTCATCGGCGGCGGCGGCGGCGG 423  
Db 809 TCAGCATGATGTTGGGTGCGACCTGCTAGCGCATGTTTCATCGGCGGCGGCGGCGGCGG 868  
QY 424 TCCAGTCTGAGTCTCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 483  
Db 869 TCCAGTCTGAGTCTCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 928  
QY 484 ACATGCTCTTCCACCAAGCTGCGAGCTGATCTTCCGCGCAGAAGATCCACGACTTATGAGC 543  
Db 929 ACATGCTCTTCCACCAAGCTGCGAGCTGATCTTCCGCGCAGAAGATCCACGACTTATGAGC 988

QY 544 ACCGTTACAGGCGCAAGATGTTTGAAGGAGCAGCATCTCGGCGGAGCTCAACGGGCCCC 603  
Db 989 ACCGTTACAGGCGCAAGATGTTTGAAGGAGCAGCATCTCGGCGGAGCTCAACGGGCCCC 1048  
QY 604 TGGGGAGGAGATCGTCAACTTCACTGCGGAGCTGGTGGCTCCATCGGCTGCTTTCG 663  
Db 1049 TGGGTGAGGAGATGTTGAACCTTCACTGCGGAGCTGGTGGCTCCATCGGCTGTTTG 1108  
QY 664 CCAACGCGCACCCCAACTTCTGTCAGCGCATGCTGACCAAGCTCAAGTTCGAGGCTTTC 723  
Db 1109 CCAATGCAACCCCAATTTCTGTCAGCGCATGCTGACCAAGCTCAAAATTTGAGGCTTTC 1168  
QY 724 AGCGGGTCACTACATCATCCGCGAAGGCAACCATCGGGAAGAGATGTATTCATCCAGC 783  
Db 1169 AGCGTGGAGATTACATCATCCGAGAGGGGACCATCCGGAAGAGATGTATTCATCCAGC 1228  
QY 784 AGCGGTGTCAGCGTCTCACTAAGGGCAACCAAGAGATGAGCTGTCGATGGCTTCT 843  
Db 1229 ATGGGTGTCAGCGTCTCACTAAGGGCAACCAAGAGATGAGCTGTCGATGGCTTCT 1288  
QY 844 ACTTCGGGAGATCTCGCTGCTCACCAGGGGCGCGCACCGGAGCTGCGGGCTGACA 903  
Db 1289 ATTCGGGAGATCTCGCTGCTCACCAGGGGCGCGGTACGGCAGGCTGCGAGCTGACA 1348  
QY 904 CCTACTGCGGCTCTTATTCGCTGAGCGTGAGCAAACTTCAACGAGGTGCTGGAGGATACC 963  
Db 1349 CCTACTGCGGCTCTTATTCGCTGAGCGTGAGCAAACTTCAACGAGGTGCTGGAGGATACC 1408  
QY 964 CCATGATGCGGCGGCTTTCGAGACCGTGGCCCATCGGCTGAGCCGCGCATCGGCAAGA 1023  
Db 1409 CCATGATGCGGCGGCTTTCGAGACTGTTGAGCTATTCACCGGCTAGATCGCATAGGCAAGA 1468  
QY 1024 AGAATTCATCTCTCTGTCACAAAGTGCAGCATGACCTCAACTC 1066  
Db 1469 AGAATTCATCTCTCTGTCACAAAGTGCAGCATGACCTCAACTC 1511

RESULT 9  
US-09-774-528-317  
; Sequence 317, Application US/09774528  
; Patent No. 6743619  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhou, Ping  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Zhang, Jie  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Xue, Aigong J.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and  
; FILE REFERENCE: 802  
; CURRENT APPLICATION NUMBER: US/09/774,528  
; CURRENT FILING DATE: 2001-01-30  
; NUMBER OF SEQ ID NOS: 441  
; SOFTWARE: pt\_fl\_genes Version 2.0  
; SEQ ID NO 317  
; LENGTH: 2976  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (18)..(2174)  
US-09-774-528-317  
Query Match 56.0%; Score 751.8; DB 4; Length 2976;



Best Local Similarity 82.6%; Pred. No. 3.5e-145; Matches 861; Conservative 0; Mismatches 182; Indels 0; Gaps 0;	
QY	4 TGGCTTACCAAGATCCTCAGCCTCCTGCGGCTGCTGCGGCTCTCACGCTGATCCGCT 63
Db	478 TTGCTTACCAAGATCCTAAGCTGCTGAGGCTGCTCGGCTCTCCGCTCATCCGCT 537
QY	64 ACATCCATCAGTGGAGAGATCTTCCACATGACCTATGACCTGGCCAGCGGGTGATGA 123
Db	538 ACATACACCATGGGAGAGATCTTTCATATGACCTATGACCTGGCCAGTGTGTGGTTC 597
QY	124 GGATCTGCAATCTCATCAGCATGATGCTGCTGCTGACCTGGGAGCGCTGCTGCAGT 183
Db	598 GCATCTTCAACCTCATTTGGATGATGCTGCTGATGTCACTGGGATGGCTGTGTGAGT 657
QY	184 TCTGTGTGCCATGCTGTCAGGAGATCTCCCGCGAACTGCTGGGTGTCCATCAATGGCATGG 243
Db	658 TCTGTGTGCCATGCTGTCAGGAGATCTCCCTCCGAGCTGCTGGGTCTCCATCAACCATGG 717
QY	244 TGAACCACTGCTGGAGTGAATCTGTAATCTCTTGGCACTCTTCAAGGCGATGAGCCATGC 303
Db	718 TGAACCACTGCTGGGCGCGCAGTATTCCTCATGCCCCTGTTCAAGGCGCATGAGCCCATGC 777
QY	304 TGTGCATCGGGTACGGCGCGGCGCGAGAGCATGACGACATCTGSGCTGACCATGC 363
Db	778 TGTGCATCGGGTATGGGCGAGCGGACCTGTAGGCACTGCCGACGTCTGGCTCACCATGC 837
QY	364 TCAGCATGATTTGGGTGGCCACCTGCTAGGCCATGTTTCATCGGCCACGCACTGCCCTCA 423
Db	838 TCAGCATGATCGTAGTGCCACATGCTAGCCATGTTTCATCGGCCATGCCCAGGCACTCA 897
QY	424 TCAGTGGCTGAGTCTCTCGCGCGCCAGTACAGAGAGAGTACAGAGAGGTGGAGCAT 483
Db	898 TCCAGTCCCTGGACTCTTCCGCGGTCACTACAGAGAGTACAGAGAGGTGGAGCAT 957
QY	484 ACATGTCCTTCCACAGCTGCCAGCTGACTTCCGCCAGAGATCCACGACTCTATGAGC 543
Db	958 ACATGTCCTTCCACAGCTGCCAGCAGACACGCGGCGAGCGCATCCACAGTACTATGAGC 1017
QY	544 ACCGTTACCAAGGCAAGATGTTTGAAGAGGACAGCATCTCGGCGGAGCTCAACGGGCCCC 603
Db	1018 ACCGTTACCAAGGCAAGATGTTTCATGAGGAAAGCATCTCGGCGAGCTGAGCGCGC 1077
QY	604 TGGGAGAGAGATCGTCAACTTCAAATGCGCGGAAGCTGTGTGGCTCCATGCGCTGTTCC 663
Db	1078 TTCGCGAGGAGATCATTAACCTTCACTGTGCGGCGCTGTGTGGCCACATGCGGCTGTTG 1137
QY	664 CCACCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
Db	1138 CCATGCGGACCCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1197
QY	724 AGCGGGGTGACTACATCATCCGCGAAGGACCATCCGCGAAGAGATGATCTTCAATCCAGC 783
Db	1198 AGCGGGGGATCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1257
QY	784 AGCGGTGTGAGCTGCTCACTAAGGGGCAACAGAGAGATGAGCTGTCCGATGGCTCCT 843
Db	1258 ATGGGTGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1317
QY	844 ACTTCGGGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 903
Db	1318 ACTTCGGGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1377
QY	904 CTTACTGCGGCTCTTATTCGCTGAGGCTGGACAACTTCAACAGAGGTGCTGGAGGATGCC 963
Db	1378 CTTACTGCGGCTTCTTACTCACTCAGGCTGGAACCATTTCAATGCTGTGCTTGGAGGTTCC 1437
QY	964 CATGATGCGGCGGCTTTCAGAGACGGTGGCCATTCGACCGCTTGGACCGGATCGGCAAGA 1023
Db	1438 CCATGATGCGGCGGCGCTTTGAGACTGTGGGCCATGATGCGGCTGCTCCGCTCGGCAAGA 1497
QY	1024 AGAATTCATCTCTTCGCAAG 1046

Db	1498 AGAATTCATCTACTGACGCGGAAG 1520
RESULT 10 US-08-997-685A-1 ; Sequence 1, Application US/08997685A ; Patent No.: 6551821 ; GENERAL INFORMATION: ; APPLICANT: The Trustees of Columbia University ; APPLICANT: Kandel, Eric ; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof ; FILE REFERENCE: 0575/54806 ; CURRENT APPLICATION NUMBER: US/08/997,685A ; CURRENT FILING DATE: 1997-12-12 ; NUMBER OF SEQ ID NOS: 60 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 1 ; LENGTH: 2733 ; TYPE: DNA ; ORGANISM: mouse US-08-997-685A-1	
Query Match 54.8%; Score 735.2; DB 4; Length 2733; Best Local Similarity 78.1%; Pred. No. 8.7e-142; Matches 884; Conservative 0; Mismatches 248; Indels 0; Gaps 0;	
QY	4 TCGCGTTTCCCAAGATTCCTCAGCCTCCTGCGGCTGCTGCGGCTCTCACGCTGATCCGCT 63
Db	737 TGAGGTTTACAAAATTTCTCAGTCTTCTGCGGTTATTACGCTTTTCAAGGTTAATCAGAT 796
QY	64 ACATCATCATCTGGGAGGAGATCTTCCACATGACCTATGACCTGGCCAGCGGGTGATGA 123
Db	797 ACATACACAGTGGGAGAGATATTCCACATGACCTATGACCTGCCAGTGTGTGGTGA 856
QY	124 GGATCTGCAATCTCATCAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183
Db	857 GGATCTTCAACTCATTTGGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 916
QY	184 TCTGCTGCGCCATGCTGACGAGTCTCCGCGCAACTGCTGGGTGCTCATTAATGGCATGG 243
Db	917 TCTGCTGCTCCCTGCTGCGAGGACTTCCCAACAGATTTGCTGGGTTTCTCTGAATGAATGG 976
QY	244 TGAACCACTCGTGGAGTGAATGTAATCTTCTCGCACTCTTCAAGGCGCATGAGCCACATGC 303
Db	977 TTAATGATTTCTGGGGAAGCAATATCTTACGCACTCTTCAAGCTATGATGATCATGC 1036
QY	304 TGTGATCGGGTACCGCGCGGAGGAGCATGACGAGCATGACGAGCATCTGGCTGACCATGC 363
Db	1037 TGTGATTTGTTATGCGCGCCCAAGCCCTGTGAGCATGCTGACCTCTGGATTACCATGC 1096
QY	364 TCAGCATGATTTGTTGGTGCACCTGCTAGCCCATGTTTATGCTGCGGCAAGGCTGCGCTCA 423
Db	1097 TGAGCATGATTTGTTGGGCGCCACTGCTACGCAATGTTTGTGTTGGCCATGCAACAGCTTTGA 1156
QY	424 TCCAGTCTGCTGACCTCTCGGCGCGCAGTACCGAGAGATGACAGAGGTGGAGCATG 483
Db	1157 TCCAGTCTTTGAGCTTTTCAAGGAGGAGTATCAAGAGAGTATTAAGCAAGTAGAGCAAT 1216
QY	484 ACATGCTCTTCCCAAGCTGCCAGCTGACTTCCGCGCAGAAAGATCCACGACTACTATGAGC 543
Db	1217 ACATGCTATTCCCAAGTTTACAGCTGACATGCGCGCAGAGATACATGATTAATGAGC 1276
QY	544 ACCGTTTACAGGCGAAGATGTTTGAAGGAGACAGCATCTCTGGCGGAGCTCAACGGGCCCC 603
Db	1277 ACCGATACCAAGGCAAGATCTTCCGATGAAGAAAATATTTCTCAGTGAGCTTAATGATCTCTC 1336
QY	604 TSCGGGAGGAGATCGTCAACTTCAACTGCGGAGCTGCTGCGCTTCCATCGGCTGTTTCG 663
Db	1337 TGAGAGAGAAATAGTCAACTTCAACTGCGGAAACTGTTGGCTACTATGCTCTCTTTTG 1396
QY	664 CCACGCGGACCCCAACTTTCGTCAGCGCATGCTGACCAAGCTCAAGTTTCGAGGTTTCC 723
Db	1397 CTAAACGCGGATCCCAATTTTGGTGACGCGCATGCTGAGCAAGCTGAGATTGAGGTTGTTCC 1456



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QY 724 AGCGGGTACTATCATCTCCGGAAGGACCACTCGGGAAGAGATGTACTTTCATCCAGC 783
DB 1457 AGCCCGGAGACTATATCATCTCGAAGAGAGCTGTGGGAAGAAATGTATTTATCCAGC 1516
QY 784 ACGGCGTGTGTCAGCTGCTCACTAAGGGCAACAAAGAGAGATGAAGCTGTCCGATGGCTCCT 843
DB 1517 ACGGTGTGTGGGTTATATCACCAGTCCAGTAAAGAAATGAAGCTGACAGATGGCTCTT 1576
QY 844 ACTTCGGGAGATCTGCTGCTCACTCCGCGGCGCGGACGCGGAGGCTGCGGGCTGACA 903
DB 1577 ACTTCGGAGAGATATGCTGCTGCTGACCAAGGCGCGGCACTGCGCAGTGTCCGAGCTGATA 1636
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DB 1817 AGGAGACGAGATCCTGAAGCAGATCGTGAAGCATGACCGGAGAGATGGTACA 1868

RESULT 11
US-09-086-436-34
; Sequence 34, Application US/09086436
; Patent No. 6703485
; GENERAL INFORMATION:
; APPLICANT: Kandel, Eric R.
; APPLICANT: Santoro, Bina
; APPLICANT: Bartsch, Dusan
; APPLICANT: Siegelbaum, Steven
; APPLICANT: Tibbs, Gareth
; APPLICANT: Grant, Seth
; TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 0575/54806-A
; CURRENT APPLICATION NUMBER: US/09/086.436
; CURRENT FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Murine
US-09-086-436-34

Query Match 52.6%; Score 706; DB 4; Length 1518;
Best Local Similarity 85.3%; Pred. No. 7.6e-136; Indels 0; Gaps 0;
Matches 787; Conservative 0; Mismatches 136;

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QY 64 ACATCCATCAGTGGAGAGATCTTCCACATGACTATGACCTGCGCAGCGCGGTGATGA 123
DB 656 ACATTCATCAGTGGGAAGAGATTTTCCACATGACTATGACCTGCGCAGCGCGGTGATC 715
QY 124 GGATCTGAATCTCATCAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 183
DB 716 GCATCGTGAACCTCATGCGCATGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 775
QY 184 TCCTGGTCCCATGCTGCGAGACTTCCCGCGCAACTGCTGGGTGTCCATCAATGGCATGG 243
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QY 244 TGAACCACTCGTGGAGTGAACCTGTACTCTCTCGCACTCTTCAAGGCCATGAGCCACATGC 303
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QY 364 TCAGCATGATTCGTGGGTGCCACTGCTAGCCATGTTTCATCGGCCACGCGCACTGCCCCTCA 423
DB 956 TCAGCATGATTCGTGGGGGCCACTGCTGTATGCCATGTTTCATCGGCCACGCGCACTGCCCCTCA 1015
QY 424 TCCAGTTCGTGGACTCTCTCGCGCGCAGTACAGGAGAAGTACAAGCAGGTGGAGCAGT 483
DB 1016 TCCAGTTCGTGGACTCTCTCGCGCGCAGTACAGGAGAAGTATAAACAAGGTGGAGCAGT 1075
QY 484 ACATGTCTTCCACAAGCTGCGAGCTGCTTCCGCGCAAGAGTCCACGACTACTATGAGC 543
DB 1076 ACATGTCTTCCACAAGCTTCCGCGCTGACACCCGACAGCGCATCCATGACTACTATGAGC 1135
QY 544 ACCGTTTACCAGGCGAAGATGTTTTCAGGAGCAGCATCTCTGGCGGAGCTCAACGGGCCCC 603
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US-08-997-685A-5
; Sequence 5, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1507
; TYPE: DNA
; ORGANISM: mouse;
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Matches 779; Conservative 0; Mismatches 132;





; CURRENT APPLICATION NUMBER: US/09/774,528  
; CURRENT FILING DATE: 2001-01-30  
; NUMBER OF SEQ ID NOS: 441  
; SOFTWARE: pt\_FL\_genes Version 2.0  
; SEQ ID NO 238  
; LENGTH: 3224  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2673)  
US-09-774-528-238

Query Match 50.7%; Score 680.2; DB 4; Length 3224;  
Best Local Similarity 75.0%; Pred. No. 1.8e-130;  
Matches 850; Conservative 0; Mismatches 283; Indels 0; Gaps 0;

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QY	184	TCCTGTGCTCCCATGCTGCAGGACTTCCCGCGCAACTGCTGGGTGCTCCATCAATGGCATGG	243
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QY	244	TGAACCACTCGTGGAGTGAATCTCTCTGCACTCTTCAAGGCCATGAGCCACATGC	303
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QY	304	TGTGCATCGGGTACGGCCGCGGAGGCGCCGAGAGCATGACGACATCTGGCTGACCATGC	363
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QY	364	TCAGCATGATGTGGGTGCGCACTGCTAGCCATGTTTCATCGCCAGCCAGCTGCGCTCA	423
Db	1130	TGAGCATGATGTGGGGGCACTGCTATGCCATGTTTGTGGCCATGCCACCGCTTTAA	1189
QY	424	TCAGTGTGCTGCACTCTCGCGCGCCAGTACACAGGAGAGTACAAGCAGGTGGAGCAGT	483
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QY	484	ACATGTCTTCCACAGCTGCCAGCTGACTTCGGCCAGAGAATCCACGACTACTATGAGC	543
Db	1250	ACATGTCTATCCATAGTTTACCAGCTGATATGCTGCGAAGATACATGATTTACTATGAAC	1309
QY	544	ACGTTTACCAGGCAAGATGTTTTCAGGAGCAGCATCTCGCGGAGCTCAACGGGCCCC	603
Db	1310	ACAGATACCAGGCAAAATCTTTGATGAGGAAATATCTCAATGAATCAATGATCTCTC	1369
QY	604	TGCGGAGGAGATCGTCAACTTCACTGCGGAAGCTGGTGGCTTCCATSCCGCTGTTTCG	663
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QY	664	CCAAAGCCGACCCCAACTTCGTTCAGGCCATGCTGACCAAGCTCAAGTTTCGAGGCTTCC	723
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QY	724	AGCCGGGTGACTACATCATCCGGAAGGACCATCGGGAAGAGATGTAATTCATCCAGC	783
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Db	1550	ACGGTGTGTGTGTCTTATCAAAAATCCAGTAAAGAAATGAAGCTGACAGATGGCTCTTT	1609

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Db	1730	CAATGATGAGGAGAGCCTTTGAGACAGTTGCCATTGACCCGACTAGATCGAATAGGAAAGA	1789
QY	1024	AGAAATTCATCTCTGACCAAGGTGACGATGACCTCAACTCGGGCGTATTTCACACAACC	1083
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QY	1084	AGGAGAACGCCATCATCTCAGGAGATCGTCAAGTACGACCGGAGATGGTGCAAG	1136
Db	1850	AGGAGAACGAAATCCTCAAGCAGATTGTGAAACATGACAGGAGATGGTGCAAG	1902

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.  
OM nucleic - nucleic search, using sw model  
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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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2	1295.4	96.5	3459	18	US-10-311-795-3	Sequence 3, Appli	
3	1295.4	96.5	3459	22	US-10-756-149-1720	Sequence 1720, Ap	
4	1207	89.9	1792	10	US-09-086-436-40	Sequence 40, Appl	
5	1207	89.9	1792	19	US-10-753-991-40	Sequence 40, Appl	
6	1194.4	89.0	1790	21	US-10-384-107-11	Sequence 11, Appl	
7	1191.6	88.8	2125	17	US-10-292-798-2011	Sequence 2011, Ap	

8	1109.2	82.7	1966	15	US-10-017-161-2369	Sequence 2369, Ap
9	1048.6	78.1	3102	14	US-10-067-457-6	Sequence 6, Appli
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11	927.2	69.1	5065	14	US-10-067-457-4	Sequence 4, Appli
12	927.2	69.1	5499	18	US-10-276-774-973	Sequence 973, App
13	874.2	65.1	1512	10	US-09-086-436-32	Sequence 32, Appl
14	874.2	65.1	1512	19	US-10-753-991-32	Sequence 32, Appl
15	871	64.9	1584	21	US-10-384-107-3	Sequence 3, Appli
16	753.4	56.1	3952	18	US-10-332-447-57	Sequence 57, Appl
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19	751.8	56.0	2325	14	US-10-158-711-9	Sequence 9, Appli
20	751.8	56.0	2976	17	US-10-120-988-317	Sequence 317, App
21	751.8	56.0	3496	18	US-10-311-795-7	Sequence 7, Appli
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23	706	52.6	1518	10	US-09-086-436-34	Sequence 34, Appl
24	706	52.6	1518	19	US-10-753-991-34	Sequence 34, Appl
25	688.8	51.3	1507	21	US-10-384-107-5	Sequence 5, Appli
26	681.8	50.8	2990	16	US-10-287-226-351	Sequence 351, App
27	680.2	50.7	1873	16	US-10-296-270-19	Sequence 19, Appl
28	680.2	50.7	1873	16	US-10-296-270-20	Sequence 20, Appl
29	680.2	50.7	2246	10	US-09-086-436-38	Sequence 38, Appl
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33	680.2	50.7	2484	16	US-10-296-270-24	Sequence 24, Appl
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35	680.2	50.7	2673	14	US-10-158-684-3	Sequence 3, Appli
36	680.2	50.7	2673	14	US-10-158-711-3	Sequence 3, Appli
37	680.2	50.7	2673	16	US-10-296-270-23	Sequence 23, Appl
38	680.2	50.7	2673	16	US-10-296-270-25	Sequence 25, Appl
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40	680.2	50.7	2748	21	US-10-466-992-3	Sequence 3, Appli
41	680.2	50.7	2748	21	US-10-466-992-13	Sequence 13, Appl
42	680.2	50.7	2748	21	US-10-466-992-15	Sequence 15, Appl
43	680.2	50.7	2748	21	US-10-466-992-17	Sequence 17, Appl
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45	680.2	50.7	2791	16	US-10-296-270-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1  
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; Sequence 2, Application US/10067457  
; Publication No. US20030082513A1  
; GENERAL INFORMATION:  
; APPLICANT: Aventis Pharma Deutschland GmbH  
; TITLE OF INVENTION: Process for identifying substances which modulate the  
; activity of hyperpolarization-activated cation channels  
; FILE REFERENCE: AVE D-2000/A006  
; CURRENT APPLICATION NUMBER: US/10/067,457  
; PRIOR FILING DATE: 2002-04-09  
; CURRENT APPLICATION NUMBER: US/09/779,587  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 3372  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-067-457-2

Query Match		96.6%	Score 1297;	DB 14;	Length 3372;
Best Local Similarity		99.0%	Pred. No. 0;		
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Db 2271 CTCGTGGGGCGCGCTGGCGCTCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2330  
QY 1322 GCACCTGCHGCCNCTCACCC 1342  
Db 2331 GCACCTGCGCGCGCTCACCC 2351

## RESULT 2

US-10-311-795-3  
; Sequence 3, Application US/10311795  
; Publication No. US20040033943A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham plc  
; TITLE OF INVENTION: New Use  
; FILE REFERENCE: P32614  
; CURRENT APPLICATION NUMBER: US/10/311,795  
; CURRENT FILING DATE: 2002-12-19  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 3459  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-311-795-3

Query Match 96.5%; Score 1295.4; DB 18; Length 3459;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 1327; Conservative 7; Mismatches 4; Indels 3; Gaps 3;

QY 4 TGGCGTTCACCAAGATCCTCAGCCCTCGCGCTCTCGCGCTCTCAGCCCTGATCCGCT 63  
Db 1030 TGGCGTTCACCAAGATCCTCAGCCCTCGCGCTCTCGCGCTCTCAGCCCTGATCCGCT 1089  
QY 64 ACATCCATCAGTGGGAGGAGATCTTCCACATGACCTATGACCTGCCAGCGCGGTATGA 123  
Db 1090 ACATCCATCAGTGGGAGGAGATCTTCCACATGACCTATGACCTGCCAGCGCGGTATGA 1149  
QY 124 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCATGCGGACGGCTGCCGTGCAGT 183  
Db 1150 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCATGCGGACGGCTGCCGTGCAGT 1209  
QY 184 TCCTGGTCCCATGCTGCAGGACTTCCCGCGCAACTGCTGGGTGTCATCAATGGCATGG 243  
Db 1210 TCCTGGTCCCATGCTGCAGGACTTCCCGCGCAACTGCTGGGTGTCATCAATGGCATGG 1269  
QY 244 TGAACCACTCGTGGAGTGAATGTAATCTCTTCGCACTCTTCAAGGCCATGAGCCACATGC 303  
Db 1270 TGAACCACTCGTGGAGTGAATGTAATCTCTTCGCACTCTTCAAGGCCATGAGCCACATGC 1329  
QY 304 TGTGATCGGGTACCGCGCGGACGGCGCCGAGAGCATGACGACATCTGGCTGACCATGC 363  
Db 1330 TGTGATCGGGTACCGCGCGGACGGCGCCGAGAGCATGACGACATCTGGCTGACCATGC 1389  
QY 364 TCAGCATGATTGGGTGCCACCTGCTAGCCATGTTTCATGGCCACCGCACTGCCCTCA 423  
Db 1390 TCAGCATGATTGGGTGCCACCTGCTAGCCATGTTTCATGGCCACCGCACTGCCCTCA 1449  
QY 424 TCCAGTCCGTGACCTCTCGCGCGCCAGTACACGAGGAAGTACAAGCAGGTGGAGCAGT 483  
Db 1450 TCCAGTCCGTGACCTCTCGCGCGCCAGTACACGAGGAAGTACAAGCAGGTGGAGCAGT 1509  
QY 484 ACATGTCTTCCACAAAGTGCAGCTGACTTCCGCGCAGGAATCCACGACTACTATGAGC 543  
Db 1510 ACATGTCTTCCACAAAGTGCAGCTGACTTCCGCGCAGGAATCCACGACTACTATGAGC 1569





Db 1990 CCATGATGGCGCGCTTCGAGACGGTGCCATGACCGCTTGACCCGATCGGCAAGA 2049  
QY 1024 AGAATTCATCTCTCTGCAACAAGGTGACGATGACCTCAACTCGGCGTATTCAACAACC 1083  
Db 2050 AGAATTCATCTCTCTGCAACAAGGTGACGATGACCTCAACTCGGCGTATTCAACAACC 2109  
QY 1084 AGAGAACGCCATCATCTCAGGAGATCGTCAAGTACGACCGGAGATGGTGACGAGCGCG 1143  
Db 2110 AGAGAACGCCATCATCTCAGGAGATCGTCAAGTACGACCGGAGATGGTGACGAGCGCG 2169  
QY 1144 AGCTGGGCTCAGCGGTGGGCTCTTTCGCCGCGCGCGCGCGCGCGCA-GTCAACCTCG 1202  
Db 2170 AGCTGGG-TCAGCGCGTGGGCTCTTTCGCCGCGCGCGCGCGCGCGCGCGCGCGCTCG 2228  
QY 1203 GCCATGCCACGCTGACGAGCGCGGCGCATGAGCTTCTGCCCGCA-GTGGCGGCGCG 1261  
Db 2229 GCCATGCCACGCTGACGAGCGCGCGCGCATGAGCTTCTGCCCGCGAGGTGGCGGCGG 2288  
QY 1262 CTCGTGGGCGCGTGGCGCTCGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1321  
Db 2289 CTCGTGGGCGCGTGGCGCTCGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2348  
QY 1322 GCACCTGCHGCNCTCAACC 1342  
Db 2349 GCACCTGCGCGCGCTCAACC 2369

RESULT 4  
US-09-086-436-40  
; Sequence 40, Application US/09086436  
; Publication No. US2003011898A1  
; GENERAL INFORMATION:  
; APPLICANT: Kandel, Eric R.  
; APPLICANT: Santoro, Bina  
; APPLICANT: Bartsch, Dusan  
; APPLICANT: Siegelbaum, Steven  
; APPLICANT: Tibbs, Gareth  
; APPLICANT: Grant, Seth  
; TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and  
; FILE REFERENCE: 0575/54806-A  
; CURRENT APPLICATION NUMBER: US/09/086,436  
; CURRENT FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 1792  
; TYPE: DNA  
; ORGANISM: Human  
US-09-086-436-40

Query Match 89.9%; Score 1207; DB 10; Length 1792;  
Best Local Similarity 99.0%; Pred. No. 9.2e-311;  
Matches 1235; Conservative 0; Mismatches 11; Indels 2; Gaps 2;  
QY 4 TGGCTTCCACCAAGATCTCAGCCTCTCGCGCTGCTCGGCTCTCAACCGCTGATCGCT 63  
Db 541 TGGCTTCCACCAAAATCTCAGCCTCTCGCGCTGCTCGGCTCTCACGCTGATCGCT 600  
QY 64 ACATCCATCAGTGGGAGGATCTCCACATGACCTATGACCTGGCGGCGGATGA 123  
Db 601 ACATCCATCAGTGGGAGGATCTCCACATGACCTATGACCTGGCGGCGGATGA 660  
QY 124 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCACTGGGACGCGCTGCGAGT 183  
Db 661 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCACTGGGACGCGCTGCGAGT 720  
QY 184 TCTGTGTCATGCTGCGAGGATCTCCCGCGCAACTGCTGGGTGTCATCAATGGCATGG 243  
Db 721 TCTGTGTCATGCTGCGAGGATCTCCCGCGCAACTGCTGGGTGTCATCAATGGCATGG 780  
QY 244 TGAACCACTCGTGGAGTGAAGTACTCTTCCACTCTTCAAGGCGCATGAGCCACATGC 303

Db 781 TGAACCACTCGTGGAGTGAAGTACTCTTCCGACTCTTCAAGGCGCATGAGCCACATGC 840  
QY 304 TGTGATCGGATPACGGCCGAGGCGCCGAGAGCATGACGAGCATATCTGGCTGACATGC 363  
Db 841 TGTGATCGGATPACGGCCGAGGCGCCGAGAGCATGACGAGCATATCTGGCTGACATGC 900  
QY 364 TCAGCATGATTTGTGGGTGCCACCTGCTAGGCGCATGTTTCATGGCCACGCCATGCCCTCA 423  
Db 901 TCAGCATGATTTGTGGGTGCCACCTGCTAGGCGCATGTTTCATGGCCACGCCATGCCCTCA 960  
QY 424 TCCAGTCTCGACTCTCTCGGCGCGCAGTAGTACCAGGAGAGTACAAAGCAGGTGGAGCAGT 483  
Db 961 TCCAGTCTCGACTCTCTCGGCGCGCAGTAGTACCAGGAGAGTACAAAGCAGGTGGAGCAGT 1020  
QY 484 ACATGTCCTTCCACAAGTTCGAGCTGACTTCCGCGCAGAAAGTCCACGACTACTATGAGC 543  
Db 1021 ACATGTCCTTCCACAAGTTCGAGCTGACTTCCGCGCAGAAAGTCCACGACTACTATGAGC 1080  
QY 544 ACCGTTACAGGGGCAAGATGTTGACGAGGACAGCATCTCGGCGAGCTCAACGGGCGCC 603  
Db 1081 ACCGTTACAGGGGCAAGATGTTGACGAGGACAGCATCTCGGCGAGCTCAACGGGCGCC 1140  
QY 604 TGGCGGAGGAGATCGTCAACTTCAACTGCCGGAAGCTGCTGCCCTTCCATGCCGCTGTCG 663  
Db 1141 TGGCGGAGGAGATCGTCAACTTCAACTGCCGGAAGCTGCTGCCCTTCCATGCCGCTGTCG 1200  
QY 664 CCAACGCGACCCCAACTTTCGTCACGCGCATGCTGACCAAGCTCAAGTTGAGAGTCTTCC 723  
Db 1201 CCAACGCGACCCCAACTTTCGTCACGCGCATGCTGACCAAGCTCAAGTTGAGAGTCTTCC 1260  
QY 724 AGCGGGGTGACTACATCATTCGCGAAGCACCATCGGAGAGAGATGATGATTTTCATCCAGC 783  
Db 1261 AGCGGGGTGACTACATCATTCGCGAAGGACCATCGGAGAGAGATGATGATTTTCATCCAGC 1320  
QY 784 AGCGGTGCTCAGCGTGTCTCACTAAGGGCAACAAGAGATGAAGTGTCCGATGCTCTCT 843  
Db 1321 AGCGGTGCTCAGCGTGTCTCACTAAGGGCAACAAGAGATGAAGTGTCCGATGCTCTCT 1380  
QY 844 ACTTCGGGAGATCTGCTGTCTCAACCGGGCGCGCGCGCAGCGAGCTGCGGGCTGACA 903  
Db 1381 ACTTCGGGAGATCTGCTGTCTCAACCGGGCGCGCGCGCAGCGAGCTGCGGGCTGACA 1440  
QY 904 CCTACTGCGGCTCTATTTCGCTGAGCGTGGACACTTCAACGAGGTGCTGGAGGAGTACC 963  
Db 1441 CCTACTGCGGCTCTATTTCGCTGAGCGTGGACACTTCAACGAGGTGCTGGAGGAGTACC 1500  
QY 964 CCATGATGCGCGCGCTTTCGAGACGCTGGCCATCGACCGCTGACCGCATCGGCAAGA 1023  
Db 1501 CCATGATGCGCGCGCTTTCGAGACGCTGGCCATCGACCGCTGACCGCATCGGCAAGA 1560  
QY 1024 AGAATTCATCTCTCTGACAAAGGTGACGATGACTCAACTCCTCGGGGCTATTCAACAACC 1083  
Db 1561 AGAATTCATCTCTCTGACAAAGGTGACGATGACTCAACTCCTCGGGGCTATTCAACAACC 1620  
QY 1084 AGGAGAACCCATCATCTCAGGAGATCTGTCAGTACGACCGGAGATGGTGACGAGGCGG 1143  
Db 1621 AGGAGAACCCATCATCTCAGGAGATCTGTCAGTACGACCGGAGATGGTGACGAGGCGG 1680  
QY 1144 AGCTGGGCTCAGCGGTGGGCTCTTTCGCGCGCGCGCGCGCGCGCGCA-GTCACTCTCG 1202  
Db 1681 AGCTGGG-TCAGCGGTGGGCTTTCGCGCGCGCGCGCGCGCGCGCGCGAGTCTACTCG 1739  
QY 1203 GCCATGCCACGCTCAGAGCGCGCGCGCATGAGCTTCTGCCCCGAG 1250  
Db 1740 GCCATGCCACGCTCAGAGCGCGCGCGCATGAGCTTCTGCCCCGAG 1787

RESULT 5  
US-10-753-991-40  
; Sequence 40, Application US/10753991  
; Publication No. US2004014242A1  
; GENERAL INFORMATION:



600	ACATCCATCAGTGGGAGAGATCTTCCACATGACCTATGACCTGGCCAGCGCGGTGATGA	659
124	GGATCTGCAATCTCATCAGCATGATGCTGCTGCTCTGCCACTGGGACGGCTGCTGCAGT	183
660	GGATCTGCAATCTCATCAGCATGATGCTGCTGCTCTGCCACTGGGACGGCTGCTGCAGT	719
184	TCCTGGTGGCCATGCTGCAGAGACTTCCGCGCAACTGCTGGGTGTCCATCATAGGCATGG	243
720	TCCTGGTGGCCATGCTGCAGAGACTTCCGCGCAACTGCTGGGTGTCCATCAATGGCATGG	779
244	TGAACCACTCGTGGAGTGAACTGTACTCTTCGCACTCTTCAAGGCCATGAGCCACATGC	303
780	TGAACCACTCGTGGAGTGAACTGTACTCTTCGCACTCTTCAAGGCCATGAGCCACATGC	839
304	TGTGCATCGGTTACGGCGCGGACGCGCCGAGAGACATGA CGGACATCTGGCTGACCATGC	363
840	TGTGCATCGGTTACGGCGCGGACGCGCCGAGAGACATGA CGGACATCTGGCTGACCATGC	899
364	TCAGATGATTTGTTGGGTGCCACTGTCTAGCGCCATGTTTCATCGGCCACGCCACTGCCCTCA	423
900	TCAGATGATTTGTTGGGTGCCACTGTCTAGCGCCATGTTTCATCGGCCACGCCACTGCCCTCA	959
424	TCCAGTGCCTGGAATCTCTCGCGGCGCCAGTACCAGGAGAGTCAACAGCAGGTGGAGCAGT	483
960	TCCAGTGCCTGGAATCTCTCGCGGCGCCAGTACCAGGAGAGTCAACAGCAGGTGGAGCAGT	1019
484	ACATGTCCTTCCACAAGCTGCCAGCTGACTTTCGCCCAGAGAGATCCAGCATCTACTATGAGC	543
1020	ACATGTCCTTCCACAAGCTGCCAGCTGACTTTCGCCCAGAGAGATCCAGCATCTACTATGAGC	1079
544	ACCGTTACACGGGCAAGATTTTGA CGAGGACAGCATCTCTGGGCGAGCTCAAACGGGCCCC	603
1080	ACCGTTACACGGGCAAGATTTTGA CGAGGACAGCATCTCTGGGCGAGCTCAAACGGGCCCC	1139
604	TGCGGAGGAGATCGTCAAATTCATCTCGCGAAGCTGTGGTCCCTCCATGCCGCTGTTCG	663
1140	TGCGGAGGAGATCGTCAAATTCATCTCGCGAAGCTGTGGTCCCTCCATGCCGCTGTTCG	1199
664	CCAAACGGGACCCCAACTTCGTCTACGGCCATGCTGACCAAGCTCAAAGTTCGAGGCTTTC	723
1200	CCAAACGGGACCCCAACTTCGTCTACGGCCATGCTGACCAAGCTCAAAGTTCGAGGCTTTC	1259
724	AGCCGGGTGATATACATCATCCGCGAAGGCACCATCGGGAAGAAGATGTACTTCATCCAGC	783
1260	AGCCGGGTGATATACATCATCCGCGAAGGCACCATCGGGAAGAAGATGTACTTCATCCAGC	1319
784	ACGGGTGGTGACGGTGTCTACTAAGGGCAACAAGGAGATGAAGCTGTCCGATGGCTCCT	843
1320	ACGGGTGGTGACGGTGTCTACTAAGGGCAACAAGGAGATGAAGCTGTCCGATGGCTCCT	1379
844	ACTTTCGGGGAGATCTGCTGCTCAACCGGGGCGCCGACGGCGAGCGTGGCGGCTGACA	903
1380	ACTTTCGGGGAGATCTGCTGCTCAACCGGGGCGCCGACGGCGAGCGTGGCGGCTGACA	1438
904	CCTACTGCGGCTCTATTTCGCTGAGCGTGGAACAATTTCAAACGAGGTGTCTGAGGAGTACC	963
1439	CCTACTGCGGCTCTATTTCGCTGAGCGTGGAACAATTTCAAACGAGGTGTCTGAGGAGTACC	1498
964	CCATGATGCGGCGGCTTTCGAGACGGTGGCCATTCGACCGGCTGGACCGCATTCGGCAAGA	1023
1499	CCATGATGCGGCGGCTTTCGAGACGGTGGCCATTCGACCGGCTGGACCGCATTCGGCAAGA	1558
1024	AGAAATTCATCTCTGACAAAGGTGACATGACCTCACTGGGCGGTATTCACCAACC	1083
1559	AGAAATTCATCTCTGACAAAGGTGACATGACCTCACTGGGCGGTATTCACCAACC	1618
1084	AGGAGAACGCCATCATCCAGGAGATCGTCAAGTACGACCGCGAGATGGTGCAGCAGGCGG	1143
1619	AGGAGAACGCCATCATCCAGGAGATCGTCAAGTACGACCGCGAGATGGTGCAGCAGGCGG	1678
1144	AGCTGGGTCAAGCGGTGGGCTCTTTCGCGCGCGCGCGCGCGCGCA-GTCACTCTG	1202
1679	AGCTGGG-TCAAGCGGTGGGCTTTTTCGCGCGCGCGCGCGCGCGCGCAGTCACTTCG	1737

Qy	1203	GCATCGCCACGCTGCAGCAGCGCGCGCCATGAGCTTCTGCCCGCAG	1250
Db	1738	GCCATCGCCACGCTGCAGCAGCGCGCGCCATGAGCTTCTGCCCGCAG	1785

  

RESULT 7	
US-10-292-798-2011	
; Sequence 2011, Application US/10292798	
; Publication No. US20030235833A1	
; GENERAL INFORMATION:	
; APPLICANT: SUWA, MAKIKO	
; APPLICANT: ASAI, KIYOSHI	
; APPLICANT: AKIYAMA, YUTAKA	
; APPLICANT: ABEURANTAN, HIROYUKI	
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS	
; FILE REFERENCE: 084335/166	
; CURRENT APPLICATION NUMBER: US/10/292,798	
; CURRENT FILING DATE: 2002-11-13	
; PRIOR APPLICATION NUMBER: 10/017,161	
; PRIOR FILING DATE: 2001-12-18	
; PRIOR APPLICATION NUMBER: JP 2001-246789	
; PRIOR FILING DATE: 2001-06-18	
; NUMBER OF SEQ ID NOS: 2070	
; SOFTWARE: PatentIn ver. 2.1	
; SEQ ID NO 2011	
; LENGTH: 2125	
; TYPE: DNA	
; ORGANISM: Homo sapiens	
; FEATURE:	
; LOCATION: source	
; FEATURE:	
; LOCATION: (1)..(2125)	
; FEATURE:	
; NAME/KEY: CDS	
; LOCATION: (201)..(1724)	
; FEATURE:	
; NAME/KEY: CDS	
; LOCATION: (1767)..(1925)	
US-10-292-798-2011	

Qy	424	TCCAGTCGCTGGACTCTCTCGGGCGCCAGGTACACAGGAGAAAGTAAACAGCAGGTGGACGAGT	483
Db	1108	TCCAGTCGCTGGACTCTCTCGGGCGCCAAATACC---AGAAGTAAACAGCAGGTGGACGAGT	1164
Qy	484	ACATGTCCTTCCACACAGCTCCGAGTCACTTCCTCGCCAGAGAGATCCACGACTACTATGAGC	543
Db	1165	ACATGTCCTTCCACACAGCTCCGGCCGACATTCGCCACAGAGATCCACGACTACTACGAGC	1224
Qy	544	ACCGTTACCAAGGGCAAGATGTTTGACGAGGACAGCATCTCTGGCGAGCTCAACCGGSCCCC	603
Db	1225	ACCGTTACCAAGGGCAAGATGTTCCAGGAGGACAGCATCCTGGCGAGCTCAACCGGSCCCC	1284
Qy	604	TGCGGGAGGAGATCGTCAACTTCACATCCGCGGAAGCTGTGTGGCTCCATGCCCGCTTTCG	663
Db	1285	TGCGGGAGGAGATGTTCAACTTCACATTCGCGGAAGCTGTGTGACTCCATGCCCGCTTTCG	1344
Qy	664	CCAAACCGGACCCCAACTTCGTTCACGCGCCATGCTGACCAAGCTCAAGTTCGAGGTCTTCC	723
Db	1345	CCAAATGCTGACCCCAACTTCGTTCAGGCCATGCTGACCAAGCTCAAGTTCGAGGTCTTCC	1404
Qy	724	AGCCGGGTGACTACATCATCCGCGAAGGCCACCATCGGGAAGAGATGTACTTCATCCAGC	783
Db	1405	AGCCGGGTGACTACCTCATCCGCGAAGGCCACCATCGG---GAAGATGTACTTCATTCAGC	1461
Qy	784	ACGCGCTGCTCAGCGTCTCTAATGAGGGCAACAGGAGATGAAGCTGTCGATGGCTCTCT	843
Db	1462	ACGCGCTGGTCAAGCTGCTCGCTAAGGGCAACAGGAGATGAAGCTGTTCGATGGCTCTCT	1521
Qy	844	ACTTCGGGGAGATCTGCTGCTCACCCGGGGCGCCGACGCGAGCGTTCGGGCTGACAC	903
Db	1522	ACTTCGGAGAGATCTGCTGCTCACCCGGGGCCACCGCATGGCGAGCTGCGGGCCACAC	1581
Qy	904	CCTACTCGCGCTCTATTTCGCTGAGCGTGGACAACTTCAACGAGGTGCTCGAGGAGTACC	963
Db	1582	CCTATTGCCGCTCTTCTTCGCTGAGCGTGGACAACTTCAACGAGGTGCTCGAGGAGTACC	1641
Qy	964	CCATGATGGCGCGGCTTTCGAGACGGTGGCCATCGACCGCTGGACCGCATCGGCACAG	1023
Db	1642	CCATGATGGCGCGGCTTTCGAGACGGTGGCCATCGACCGCTGGACCGCATCGGCACAG	1701
Qy	1024	AGAAATCCATCCTCTGCACAAAGTGCAGCATGACCTCAACTCGGGCGGTATTCAACAACC	1083
Db	1702	AGAAATCCATCCTCTGCACAAAGTGCAGCATGACCTTAACTCGGGCGGTATTCAACAACC	1761
Qy	1084	AGGAGAACGCCATCATCCAGGAGATCGTCAAGTACGACCGGAGATGGTCCAGCAGCGCG	1143
Db	1762	AGTAGAACGCCATCATCCAGGAGATCGTCAAGTACGACCGGAGATGGTCCAGCAGCGCG	1821
Qy	1144	AGCTGGGCTCAGCGGTGGGCTCTTCCGCGCGCGCGCGCGCGCGCGCAGTCACTCTCG	1203
Db	1822	AGCTGGG---TCACGCGCTGGGCTCTTCCGCGCGCGCGCGCGCGCAG---GTCACTCTCG	1878
Qy	1204	CCATCGCACCGCTCGACGAGCGGGCGGCATGACTTCTGCCCGCA---GTGGCGGGCGCG	1262
Db	1879	CCATCGCACCGCTCGACGAGCGCGGTGTCATGAGCTTCTGCCCGCAGAGTGGCGGGCGCG	1938
Qy	1263	TCGTGGGCGCGTGGCGCTCGGCTCGCGCGCTCTGTCGCGHGCYNDYHCCCGGGGSCCG	1322
Db	1939	TCGTGGGCGCGTGGCGCTCGGCTCGCGCGCTCTGTCGCGCGCTCTGTCGCGCGCGCGCG	1998
Qy	1323	CACCTGHHGCNCCTCAACC	1342
Db	1999	CACCTGCGCGGCTCAACC	2018

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: APPLICANT: AURATANI, HIROYUKI
:
: TITLE OR INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
:
: FILE REFERENCE: 084335/0152
:
: CURRENT APPLICATION NUMBER: US/10/017,161
:
: CURRENT FILING DATE: 2002-12-18
:
: PRIOR APPLICATION NUMBER: JP 2001/246789
:
: PRIOR FILING DATE: 2001-06-18
:
: NUMBER OF SEQ ID NOS: 2430
:
: SOFTWARE: PatentIn Ver. 2.1
:
: SEQ ID NO 2369
:
: LENGTH: 1366
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: FEATURE:
:
: NAME/KEY: source
:
: LOCATION: (1)..(1966)
:
: FEATURE:
:
: NAME/KEY: CDS
:
: LOCATION: (201)..(1766)
:
: FEATURE:
:
: NAME/KEY: modified_base
:
: LOCATION: (7)..(106)
:
: OTHER INFORMATION: a, t, c, g, unknown or other
:
: FEATURE:
:
: NAME/KEY: modified_base
:
: LOCATION: (139)
:
: OTHER INFORMATION: a, t, c, g, unknown or other
:
: FEATURE:
:
: NAME/KEY: modified_base
:
: LOCATION: (1915)..(1966)
:
: OTHER INFORMATION: a, t, c, g, unknown or other
:
: JS-10-017-161-2369

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Query Match	82.7%;	Score 1109.2;	DB 15;	Length 1966;
Best Local Similarity	95.8%;	Pred. No. 9.6e-285;		
Matches 1184: Conservative	0;	Mismatches 43;	Indels 9;	Gaps 4;

RESULT 8  
US-10-017-161-2369  
; Sequence 2369, Application US/10017461  
; Publication No. US20030143668A1  
; GENERAL INFORMATION:  
; APPLICANT: SUWA, MAKIKO  
; ASAI, KIYOSHI  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA

QY 544 ACCGTTACAGGCGAAGATGTTTTCAGAGGACAGCATCTGCGGAGCTCAACGGGCCCC 603  
DB |||||  
QY 1225 ACCGTTACAGGCGAAGATGTTTTCAGAGGACAGCATCTGCGGAGCTCAACGGGCCCC 1284  
DB |||||  
QY 604 TCGGGAGGAGATCGTCAACTTCAACTGCGGGAAGCTGGTGGCTCCATGCGGCTGTTTCG 663  
DB |||||  
QY 1285 TCGGGAGGAGATGTTCAACTTCAACTGCGGGAAGCTGGTGGCTCCATGCGGCTGTTTCG 1344  
DB |||||  
QY 664 CCAACGCGACCCCAACTTTCGTACGCGCATCTGACCAAGCTCAAGTTGAGAGTCTTCC 723  
DB |||||  
QY 1345 CCAATGCTGACCCCAACTTTCGTACGCGCATCTGACCAAGCTCAAGTTGAGAGTCTTCC 1404  
DB |||||  
QY 724 AGCGGTTGACTACATCATCCCGAGGACCATCGGAGAGATGATGTTCAATCCAGC 783  
DB |||||  
QY 1405 AGCGGTTGACTACATCATCCCGAGGACCATCGGAGAGATGATGTTCAATCCAGC 1461  
DB |||||  
QY 784 AGCGGTTGCTCAGCGTGTCTCACTAAGGGCAACAGGAGATGAAGTGTCCGATGGCTCCT 843  
DB |||||  
QY 1462 AGCGGTTGCTCAGCGTGTCTCGCTAAGGGCAACAGGAGATGAAGTGTTCGATGGCTCCT 1521  
DB |||||  
QY 844 ACTTCGGGAGATCTGCTGTCTCAACCGGGGCGGCGACGCGAGCGTGGGGGTGACA 903  
DB |||||  
QY 1522 ACTTCGGGAGATCTGCTGTCTCAACCGGGGCGGCGACGCGATGCGAGTGTGGGGCAACA 1581  
DB |||||  
QY 904 CCTACTGCGGCTCTATTTCGCTGAGCGTGACCACTTCAACGAGTGTGGAGGAGTACC 963  
DB |||||  
QY 1582 CCTATTGCGGCTCTCTTTCGCTGAGCGTGGACAACCTTCAACGAGTGTGGAGGAGTACC 1641  
DB |||||  
QY 964 CATGATGCGGCGCGCTTTCGAGACGCTGGCCATCGACCGCTGGACCGCATCGGCAAGA 1023  
DB |||||  
QY 1642 CATGATGCGGCGCGCTTTCGAGACGCTGGCCATCGACCGCTGGACCGCATCGGCAAGA 1701  
DB |||||  
QY 1024 AGAATTCATCTCTCTGCAACAGGTGACGATGACCTCAACTCGGGCGTATTCAACAACC 1083  
DB |||||  
QY 1702 AGAATTCATCTCTCTGCAACAGGTGACGATGACCTTAACTCGGGCGTATTCAACAACC 1761  
DB |||||  
QY 1084 AGGAGAACCCATCATCCAGGAGATCGTCAAGTAGACGCGGAGATGTGACGAGGCGG 1143  
DB |||||  
QY 1762 AGTAGAACCCATCATCCAGGAGATCGTCAAGTAGACGCGGAGATGTGACGAGGCGG 1821  
DB |||||  
QY 1144 AGCTGGGCTCAGCGGCTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGAG 1203  
DB |||||  
QY 1822 AGCTGGG-TGGGCGCTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGAG--GTCACTCGG 1878  
DB |||||  
QY 1204 CCATGCCACGCTGACGAGGCGGCGCGCATGAGCT 1239  
DB |||||  
QY 1879 CCATGCCACGCTGACGAGGCGGCGGTGTCATGAGCT 1914  
DB |||||

RESULT 9  
US-10-067-457-6  
; Sequence 6, Application US/10067457  
; Publication No. US20030082513A1  
; GENERAL INFORMATION:  
; APPLICANT: Aventis Pharma Deutschland GmbH  
; TITLE OF INVENTION: Process for identifying substances which modulate the  
; FILE OF INVENTION: activity of hyperpolarization-activated cation channels  
; FILE REFERENCE: AVE D-2000/A006  
; CURRENT APPLICATION NUMBER: US/10/067,457  
; CURRENT FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: US/09/779,587  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 3102  
; TYPE: DNA  
; ORGANISM: Murinae gen. sp.  
US-10-067-457-6

Query Match 78.1%; Score 1048.6; DB 14; Length 3102;  
Best Local Similarity 87.6%; Pred. No. 1.4e-268;  
Matches 1173; Conservative 6; Mismatches 156; Indels 4; Gaps 3;

QY 4 TGGCGTTACCAAGATCTCTAGCCCTCTGCGGCTGCTGCGCTCTCAGCGCTGATCCGCT 63  
DB |||||  
QY 931 TGGCGTTACCAAGATCTCTAGCTCTGCTGCGCTGCTGCGCTATCAGGCTCATCCGAT 990  
DB |||||  
QY 64 ACATCCATCAGTGGGAGAGATCTTCCACATGACCTATGACCTGCGCCAGCGGCTGATGA 123  
DB |||||  
QY 991 ATATCCACAGTGGGAGAGATTTTCCACATGACCTACGACCTGGCAAGTGCAGTGATGC 1050  
DB |||||  
QY 124 GGATCTGCAATCTCATCAGCANTGATGCTGCTGCTGCTGCTGCGCATGGGACGGCTGCTGCAGT 183  
DB |||||  
QY 1051 GCATCTGTAACTCTGATCAGCATGATGCTACTGCTCTGCTGCTGCTGCGGACGGTTCCTGCAGT 1110  
DB |||||  
QY 184 TCCTGGTGGCCATCTGTCAGGACCTTCCCGGCAACTGCTGGGTGCTCCATCAATGGCATGG 243  
DB |||||  
QY 1111 TCCTGGTGGCCATCTGTCAGACTTCCCGAGGACTGCTGGGTGCTCCATCAACACATGG 1170  
DB |||||  
QY 244 TGAACCACTCGTGGAGTGAATGTACTCTCTTCGCACTCTTCAAGGCCATGAGCCATGTC 303  
DB |||||  
QY 1171 TGAACCACTCGTGGAGCGAGCTCTACTCTGTTGCGCTCTTCAAGGCCATGAGCCATGTC 1230  
DB |||||  
QY 304 TGTGATCGGTAACGCGCGGAGGCGGCGGAGAGATGACGAGATCTGGGCTGACCATGTC 363  
DB |||||  
QY 1231 TGTGATCGGTAACGCGCGGAGGCGGCGGAGAGATGACGAGATCTGGGCTGACCATGTC 1290  
DB |||||  
QY 364 TCAGCATGATTTGGTGGTGCACCTGCTACGCCATGTTTCATCGGCACGCCACTGCGCTCA 423  
DB |||||  
QY 1291 TCAGCATGATGTTAGGGGCGGCGGCTGCTATGCTGCTCTTTCATGGGCGGCGGCTGCTCA 1350  
DB |||||  
QY 424 TCCAGTCTGCTGCACTCTCTCGCGGCGGCGGAGTACAGGAGAGTACAAAGCAGGTGGAGCAT 483  
DB |||||  
QY 1351 TCCAGTCTGCTGATTTGCTACGCGGCGGCGGAGTACAGGAGAGTACAAAGCAGGTGGAGCAT 1410  
DB |||||  
QY 484 ACATGCTCTTCCACAGCTGCGGAGTGTGCTGCTGCGGAGAGATGCAAGCTACTATGAGC 543  
DB |||||  
QY 1411 ACATGCTCTTCCACAAACTGCGCGCTGCTACTTCCGCGAGAGATCCACGATTTACTATGAGC 1470  
DB |||||  
QY 544 ACCGTTACCAAGGCAAGATGTTTTCAGGAGGACAGCATCTGCGGAGCTCAACGGGCCCC 603  
DB |||||  
QY 1471 ACCGTTACCAAGGCAAGATGTTTTCAGGAGGAGATGTTTTCAGGAGGAGATGTTTTCAGGAGGAG 1530  
DB |||||  
QY 604 TGGCGGAGGAGATCGTCAACTTCAACTGCGCGGAGCTGGTGGCTTCCATGCGGCTGTTTG 663  
DB |||||  
QY 1531 TGGTGGAGGAGATGTTGAGACTTCAACTGCGCGGAGCTGGTGGCTTCCATGCGGCTGTTTG 1590  
DB |||||  
QY 664 CCAACGCGGACCCCAACTTTCGTCAGGCGCATGCTGACCAAGCTCAAGTTGAGAGTCTTCC 723  
DB |||||  
QY 1591 CCAATGACAGACCCCAACTTTCGTCAGGCGCATGCTGACAAAGCTCAAAATTTGAGGCTTCTCC 1650  
DB |||||  
QY 724 AGCGGTTGACTACATCATCCCGGAGGCGGAGGAGATGATGTTCAATCCAGC 783  
DB |||||  
QY 1651 AGCGTTGAGATTTACATCATCCGAGAGGAGGAGGAGATGATGTTCAATCCAGC 1710  
DB |||||  
QY 784 AGCGGTTGCTCAGCGTGTCTCACTAAGGCGCAACAGGAGATGAAGCTGCTCCGATGGCTCCT 843  
DB |||||  
QY 1711 ATGGGTTGCTGAGCGTGTCTCAACAGGCGCAACAGGAGATGAGCTGTCGATGCTCCT 1770  
DB |||||  
QY 844 ACTTCGGGAGATGCTGCTGCTCAACCGGGGCGGCGGAGCGGCGGAGCGTGGGGCTGACA 903  
DB |||||  
QY 1771 ATTTTCGGGAGATCTGCTTGTCTCAGAGGGGCGGCGGTACGCGGCGGAGCTGAGCTGACA 1830  
DB |||||  
QY 904 CCTACTGCGGCTCTATTTCGCTGAGCGTGGAGCAACTTCAACAGGAGTGTGGAGGAGTACC 963  
DB |||||  
QY 1831 CCTACTGCGGCTCTACTCTACTGAGTGGAGCAATTTCAACAGGAGTGTGGAGGAGTACC 1890  
DB |||||  
QY 964 CCATGATCGGCGGCGCTTTCGAGACGCTGGGCGCATCGACCGCTGAGCGCATCGGCAAGA 1023  
DB |||||  
QY 1891 CCATGATCGGCGGCGCTTTCGAGACTGTGGCTATTGACCGGCTAGATCGCATAGGCAAGA 1950  
DB |||||  
QY 1024 AGAATTCATCTCTCTGCAACAGGTGACGATGACCTCAACTCGGGCGGCTATTCACCAACC 1083  
DB |||||  
QY 1951 AGAATTCATCTCTCTGCAACAGGTTCAGATGATCTCAGCTCAGGCTGTGTTTCAACAACC 2010  
DB |||||





; ORGANISM: Homo sapiens		69.1%; Score 927.2; DB 14; Length 5065;	
US-10-067-457-4		Best Local Similarity 84.7%; Pred. No. 2.9e-236;	
		Matches 1040; Conservative 0; Mismatches 188; Indels 0; Gaps 0;	
QY	4	TGGCTTACCAAGATCCTCAGCCTCTCGGGCTGCTGGCTCTCAAGCCTGATCCGCT	63
Db	1696	TGGCTTACCAAGATCCTCAGCCTCTTACGGCTGTACGGCTCTCCCGCCTCAATTCGAT	1755
QY	64	ACATCCATCAGTGGGAGGAGATCTCCACATGACCTATGACCTGGCGACGGGGTATGA	123
Db	1756	ATATTACCAAGTGGGAGGAGATCTTCCATGACCTTACGACCTGGCGACGGCGTGGTGC	1815
QY	124	GGATCTGCAATCTCATCAGATGATGCTGCTCTGCGCACTGGGACGGCTGCTGCACT	183
Db	1816	GCATCGTGAACCTCATCGGCATGATGCTCTGCTCTGCCACTGGGACGGCTGCTGCACT	1875
QY	184	TCTGTGTCCTGCTGCGAGGATTCGCGGCACTGCTGGGTGTCCATCAATGGCATGG	243
Db	1876	TCTGTGTCCTGCTGCGAGGATTCGCGGCACTGCTGGGTGTCCATCAATCAACATGG	1935
QY	244	TGAACCACTCGTGGAGTGAATGTACTCTTCCGCACTCTTCAAGGCCATGAGCCACATGC	303
Db	1936	TGNACCACTCTGGGGAAGCAGTACTCTACGGCTCTTCAAGGCCATGAGCCACATGC	1995
QY	304	TGTGATCGGGTACGCGCGGACGGCGCCGAGAGCATGACGACATCTCGCTGACCATGC	363
Db	1996	TGTGATCGGCTACGCGCGGACGGCGCCGAGGATGTCGAGCTGCTGGCTCACCATGC	2055
QY	364	TGAGCATGATTTGGGTGCCACTGCTAGCCCATGTTTATCGGCCACGGCACTGCCCTCA	423
Db	2056	TCAGCATGATCGTGGGTGCCACTGCTAGCCCATGTTTATGGCCACGGCACTGCCCTCA	2115
QY	424	TCAGTCTGCTGACTCTCGCGCGCAGTACAGGAGAAAGTACAGAGAGTGGAGCAGT	483
Db	2116	TCAGTCTGCTGACTCTCGCGCGCAGTACAGGAGAAAGTACAGGAGTGGAGCAGT	2175
QY	484	ACATGTCTTCCACAAAGCTGCCAGCTGACTTCGCGCAGAGATCCACGACTACTATGAGC	543
Db	2176	ACATGTCTTCCACAAAGCTGCCAGCTGACTTCGCGCAGAGATCCACGACTACTATGAGC	2235
QY	544	ACGTTACAGGCAAGATGTTTGACGAGGACAGCATCTGGCGAGGCTCAACGGGCCCC	603
Db	2236	ACGCTACAGGCAAGATGTTTGACGAGGAGGATCTCGCGAGGATCTCGCGAGGCTTCC	2295
QY	604	TGCGGAGGAGATCGTCAACTTCACTGCGGGAAGCTGGTGGCTTCCATGCGCTGTTGG	663
Db	2296	TGCGGAGGAGATCATCAACTTAACTGTCGAGAGTGGTGGCTTCCATGCGCTGTTGG	2355
QY	664	CCAAACCGACCCCACTTCTGTCACGGCCATGCTGACCAAGCTCAAGTTGAGGTTTCC	723
Db	2356	CCAAATCGGACCCCACTTCTGTCACGGCCATGCTGACCAAGCTGCGTTTCGAGGCTTCC	2415
QY	724	AGCGGGTGAATCATATCCGGGAAGGACCATCCGGGAAGAGATGTAATTCATCCAGC	783
Db	2416	AGCTGGGAGCTACATCATCCGGGAAGGACCATTTGGCAAGAGATGTAATTCATCCAGC	2475
QY	784	AGCGGTGTGTCAGCTGCTCACTAAGGGCAACAGGAGATGAAGCTGTCGGATGGCTCT	843
Db	2476	ATGGCTGTGTAGCTGCTCACTAAGGGCAACAGGAGATGAAGCTGTCGGATGGCTCT	2535
QY	844	ACTTCGGGGAGATCTGCTGCTCACCCTGGGGCGCGCACGGGAGCGTGGGGGTGACA	903
Db	2536	ACTTTGAGAGATCTGCTGCTGACCCGGGGCGCGCACAGCGGTGAGGGCGGACA	2595
QY	904	CTTACTGCGGCTCTATTCTGCTGAGCGTGGACAATTTCAACAGAGGTGCTGGAGGATACC	963
Db	2596	CCTACTGCGGCTCTTACTGCTGAGCGTGGACAATTTCAATGAGGTGCTGGAGGATACC	2655
QY	964	CCATGATGGGGCGCTCTTGAGAGCGGTGGCCATCGACCGCTGGAGCGCATCGGCAAGA	1023

RESULT 12

US-10-276-774-973

Sequence 973, Application US/10276774

Publication No. US20040053245A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

APPLICANT: Tang, Y, Tom et al

TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides

FILE REFERENCE: 21272-030

CURRENT APPLICATION NUMBER: US/10/276,774

CURRENT FILING DATE: 2002-11-18

PRIOR APPLICATION NUMBER: 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 09/496,914

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 2700

SOFTWARE: Custom

SEQ ID NO 973

LENGTH: 5499

TYPE: DNA

ORGANISM: Homo sapiens

US-10-276-774-973

Query Match 69.1%; Score 927.2; DB 18; Length 5499;

Best Local Similarity 84.7%; Pred. No. 3e-236;

Matches 1040; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 4 TGGCTTACCAAGATCCTCAGCCTCTCGGGCTGCTGGCTCTCAAGCCTGATCCGCT 63

Db 2128 TCGCTTACGAAGATCTCAGCCTCTTACGGCTCTTACGGCTCTCCCGCTCATTCGAT 2187

QY 64 ACATCCATCAGTGGGAGGAGATCTTCCACATGACCTATGACCTGGCGAGCGGGTATGA 123

Db 2188 ATATTACCAAGTGGGAAGAGATCTTCCACATGACCTAGACCTGGCCAGCGCGTGGTGC 2247

QY 124 GGATCTGCAATCTCATCAGCATGATGCTGCTGCGCACTGCGACCTGGACCGCTGCTGCACT 183

Db 2248 GCATCGTGAACCTCATCGGCATGATGCTCTGCTGCTGCGACCGCTGCTGCACT 2307

QY 184 TCCTGTGTCCTATGCTGAGGACTTCCCGCGCAACTGCTGGGTGTCCATCAATGGCATGG 243

Db 2308 TCCTGTGTCCTATGCTGAGGACTTCCCTGAGCATGCTGGGTGTCCATCAACACATGG 2367

QY 244 TGAACCACTCGTGGAGTGAATGTACTCTTTCGCACTCTTTCAAGGCCATGAGCCACATGC 303

Db 2368 TGAACCACTCTGGGGGAAGCAGTACTCTTACGGCTCTTCAAGGCCATGAGCCACATGC 2427

QY 304 TGTGATCGGGTACGGCGGCGGAGAGATGACGACATCTGGCTGAGCCATGC 363

Db 2428 TGTGATCGGGTACGGCGGCGGAGGCGCGGTGGGATGTCGAGCATGCTGGCTCACCATGC 2487

QY 364 TCAGCATGATTTGGGTGCCACTGCTAGCCCATGTTTATCGGCCACGGCACTGCCCTCA 423

Db 2488 TCAGCATGATCGTGGGTGCCACTGCTAGCCCATGTTTATGGCCACGGCACTGCCCTCA 2547









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